GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

using sw model protein search, OM protein - Search time 59 Seconds (without alignments) 4635.127 Million cell updates/sec August 25, 2004, 17:06:26; Run on:

US-09-442-489F-2 14575 1 MAAASYDQLLKQVEALKMEN.......ESSGTQSPKRHSGSYLVTSV 2843 Title: Perfect score:

Sequence:

Scoring table:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

Database

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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RESULT	-

adenomatous polyposis coli protein - human NyAlternate names: polyposis coli locus protein DP2.5; tumor suppressor APC Cipacies: Homo sapiens (man) Cipacies: Homo sapiens (man) Cipacies: J1-Dec-1991 #sequence revision 31-Dec-1991 #text\_change 21-Jul-2000 Cipacission: A37261; B39658; A44928; A49319; I54271 R.Kinzler, K.W.; Milbert, M.C.; Su, L.K.; Vogelstein, B.; Bryan, T.M.; Levy, D.B.; Smith, Science 253, 661-665, 1991 A.Fitle: Identification of FAP locus genes from chromosome 5q21. A.Reference number: A37261; MulD:91335210; PMID:1651562

A; Molecule type: mRNA A; Molecession: A3726; Millo 1982396; PIDN:AAA01586.1; PID:G182397 A; Molecule type: mRNA A; Molecule type: Mr. thisveris, A: Alberteen, H: Gelbert, L: Samowitz, W.; Grode arrington, J.; Molecule M: Thisveris, A: Alberiers at the familial polypos A; Molecesion: mB3658 MUD:13103037; PMD:1673319 A; Molecule type: DNA A; Molecesion: Mishishor, I: Horit, A: Miyoshi, Y: Utsunomiya, J: Kinzler, K.W.; Vogelste A; Mixle: DNA A; Molecule type: DNA A; Molecule

C,Genetics: A,Genes: GDB:A,Cross-cobe: GDB:A,Nap Position A,Nap Position A,Note: mutat C,Superdamily C,Keywords: C,F,1-73/Comai: F,1-73/Comai: F,1-131/202/Region F,1131-1156/R,F;1558-1577/RF;F;1558-1577/RF;F;F;F;F;F;F;F;F;F;F;F;F;F;F;F;F;F;F;	;Genetics: GDB:APC GGENE: GDB:119682; OMIM:175100  Map position: 5q21-5q22  NOte: mutations of this gene can result in familial adenomatous polyposis or sporadic NOte: mutations of this gene can result in familial adenomatous polyposis coli protein Note: mutations of this gene can result in familial adenomatous polyposis or sporadic Note: mutations of this gene can result in familial adenomatous polyposis, tumor suppressor 1-730/Domain: leucine-rich NTD> 1-730/Domain: leucine-rich ATD> 1-732/Region: coll #status predicted 1-731-2832/Domain: scrine-rich cCTD> 1-131-1156/Region: acidic 1-131-1156/Region: acidic 1-13858-12577/Region: highly charged	6 6 6 6 6 6 6	PKASHRSKQRHKQSLYGDYVPDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSSRG LDSSRSBEKDRSLERRGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVWEBVSALHT LDSSRSBEKDRSLERRERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVWEBVSALHT QBDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRS QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRS QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRS NDSLNSYSSSDGYRGQMKPSIESYSBDBSKFCSYGGYPADLAHKIHSANHDDNDG NDSLNSYSSSDGYGKRQMKPSIESYSBDBSKFCSYGGYPADLAHKHSANHMDDNDG NDSLNSYSSSDGYGKRQMKPSIESYSBDBSKFCSYGGYPADLAHKHSANHMDDNDG
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3 8 8	VDCEMYGLINDHYSITLRRYAGMALTNLFGDVANKATLCSMKGCMRALVAQLKSESEDL 5	y d	1561 KDLLDDSDDDIBILEECIISAMPTKSSRKGKKPAQTASKLPPPVARKPSQLPVYKLLPS 1620 
8 8 8	VDCEMYGLINDHYSITLKKYAGRALINDHYGDVARKATLCSKKGCMKALVAQLKSBSEDL S QQVIASVLRNLSWRADVNSKKTLREVGSVKALMBCALEVKKESTLKSVLSALMNLSAHCT 6	oy Oy	1621 QNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 1680
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#text\_change 13-Aug-1999 149505
adenomatous polyposis coli protein - mouse
N,Alternate names: APC
C,Species: Mus musculus (house mouse)
C,Date: 02-Uul-1996 #sequence\_revision 02-Jul-1996 :
C,Accession: 149505 RESULT

10, LDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTS OTDLTRRQLEYEARQIRVAMEEQLGTCQDMEXRAQRRIARIQQIEKDILRIRQLLQSQAT WEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQ QOVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWNLSAHCT CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSKHKMIAM GSAAALRNIMANRPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLS PKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSSRGS EAERSSONKHETGSHDAERONEGOGVGEINWATSGNGOGSTTRMDHETASVLSSSSTHSA RIFVNGSRESTGYLEELEKERSLILADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL HGNDKDSVLLGNSRGSKEARARARALHNI IHSQPDDKRGRREIRVLHLLBQIRAYCETC ASSGOIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR RGFVNGSRESTGYLBELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL PRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLLAMSSSQDSCISMRQSGCLPLLIQLL MAAASYDQLLKQVEALKMENSNIRQELEDNSNHLTKLETEASNMKEVIKQLQGSIBDEAM Gaps PID:9191992 2845; RiSu, L. Science 256, 668-670, 1992
Science 256, 668-670, 1992
A;Title: Multiple intestinal neoplasia caused by a mutation in A;Reference number: 149505; MUID:92263101; PMID:1350108
A;Accession: 149505
A;Rotatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2445 <RES>
A;Cross-references: GB:M88127; NID:g191991; PIDN:AABS9632.1; PI
C;Superfamily: adenomatous polyposis coli protein Length Indels ñ 159; DB Query Match 90.2%; Score 13148; Best Local Similarity 90.0%; Pred. No. 0; Matches 2566; Conservative 113; Mismatches н 25 B S B 6 B 6 8 & 8 \$ B \$ 요 상 임 8 8 8 \$ B \$ 8 6 8 8 8 8 ò

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A;Accession: T30258 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1.2274 <van> A;Residues: 1.2274 <van> C;Genetics: EMBL:AJ130783; NID:g4210431; PIDN:CAA10207.1; PID:g4210432 A;Genetics: A;Gene: APC2 A;Introns: 47/3; 78/1; 138/2; 174/3; 212/3; 238/3; 271/3; 396/1; 428/1; 474/3; 500/3; 53</van></van>	Query Match  24.1%; Score 3508.5; DB 2; Length 2274;  Best Local Similarity 34.4%; Pred. No. 1.7e-136;  Matches 1005; Conservative 356; Mismatches 789; Indels 773; Gaps 98;  4 ASYDQLIKQVEALKMENSNIRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAMA 61	62 SGGOIDLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGGCSPVPMGSFPRR 121	H 80 47		LGGLGAVAEELLQVDYEMHKMIKLPINNALKKIAGMITINNITFGVANAAILCAKKGCMEA LVAQLKSESEDLQQVIASVIRNLSWRADVNSKKTIREVGSVKALMECALEVKKESTIKKSV	LISALMNISAHSITENKAAICQVDGALGFUVSIDITINCQGSSLAVEESGGGLIMANGAVSMIKA NEDHRQILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLK   :  :  :	

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A;Reference number: Z17782; MUID:97144426; PMID:8990193 A;Accession: T11882 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-2416 <hay> A;Centics: A;Genetics: EMBL:U77947; NID:g1800228; PID:g1800229; PIDN:AAB41404.1 C;Genetics: A;Gene: D-APC A;Cross-references: FlyBase:FBgn0015589 A;Map position: 3R</hay>	Query Match 12.2%; Score 1778.5; DB 2; Length 2416; Best Local Similarity 25.5%; Pred. No. 2.8e-65; Matches 721; Conservative 330; Mismatches 845; Indels 935; Gaps 101	QY 243 ERSSQNKHETGSHDAERQN-EQGYGEINWATSGNGGGSTTRMDHETASVLSSS 295   :   :	Qy	QY         338         SSSQDSCISWRQSGCLPLLIQLLHGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDD         397           L	QY 398 KRGRREIRVLHLLEQIRAYCETCWEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMK 455	QY 456 LSFDEERHAANNELGGLQAIAELLQVDCEMYG-LTNDHYSITLRRYAGMALTNLTFGDVA 514	Qy 515 NKATLCSMKGCMRALVAQLKSESEDLQQYIASVLRNLSWRADVNSKKTLREVGSVKALME 574	OY 575 CALBVKKESTLKSVLSALMNLSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIES 634	QY 635 GGGILRNVSSLIATNEDHRQILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKD 694	Qy 695 QEALWDMGAVSMLKNLIHSKHKMIAMGSAAALRNLMANRPAKYKDANIMSPG-SSL 749	Qy 750 PSLHVRKQKALEAELDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYVFDTNRHDDN 809  :	QY 810 RSDNFNTGNMTVLSPYLNTTVLFSSSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATEN 869	QY         870 PGTSSKRGLQISTTAAQIAKVMEEVSAIHTSQEDRSGSTTELHCVTDERNALRRSSAAH 929           I   <td< th=""><th>O. THE CAMPANIES TO THE CAMPANIES TO THE TAXABLE TO</th></td<>	O. THE CAMPANIES TO THE CAMPANIES TO THE TAXABLE TO
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12.2%; Score 1778.5; DB 2; Length 2416;
coal Similarity 25.5%; Pred. No. 2.8e-65;
721; Conservative 330; Mismatches 845; Indels 935; Gaps 101; 514 DESKFCSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNSGRQSPSQNERW 1049 1050 ARPKHIIEDEIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQQECVSPYRSRGANG 1109 337 397 298 455 409 469 589 749 649 574 634 529 694 PSIHVRKOKALEAELDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYVFDTWRHDDN 809 677 869 695 734 749 930 THSNTYNFTKSENSNRTCSMPYAKLEYKRSSNDSLNSVSSNDGYGKRGOMKPSIESYSED 989 296 STHSAPR-----RLTSH-----LGTKVEMVYSLLSMLGTHDKDDMSRTLLAM 243 ERSSQNKHETGSHDAERQN-EGQGVGEINMATSGNGQGSTTR-----MDHETASVLSSS KRGRREIRVLHLLEQIRAYCETCWEWQEAHEPGM--DQDKNPMPAPVEHQICPAVCVLMK 299 KAGRREAKVLRLLDQIVDYCSFLKTLLQSGGBAIADDSDRHPL-----AAISSLMK 350 VSFDEEHRHAMCELGALHAIPNLVHLDHAVHGPKPEDQCCNSLRRYALMALTNLTFGDEN SSSQDSCISMRQSGCLPLLIQLLHGNDKDSVLLGNSRGSKEARARASAALHNIHSQPDD 456 LSFDEEHRHAMNELGGLQALAELLQVDCEMYG-LTNDHYSITLRRYAGMALTNLTFGDVA 410 NYALLCGQKQFMEALVAQLDSAPDDLLQVTASVLRNLSWRADSNMKAVLNEIGTVTAIAL 575 CALEVKKESTLKSVLSALMNLSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIES 530 AGGILRNVSSHIAVCEPYRQILRQHNCLAILLQQLKSESLTVVSNSCGTLWNLSARSAED RSDNFNTGNMTVLSPYLNTTVLPSSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATEN 515 NKATLCSMKGCMRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLREVGSVKALME 695 QEALWDMGAVSMLKNLIHSKHKMIAMGSAAALRNLMANRPAKYK----DANIMSPG-SSL -----KLDKERASSSSRRHP----870 PGTSSKRGLQISTTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCVTDERNALRRSSAAH 635 GGGILRNVSSLIATNEDHRQILRENNCLQTILQHLKSHSLTIVSNACGTLWNLSARNPKD PTLEARKAKALQQELGERHTAETCDNLD-------------ODTEATEBOPIDYSVKYS------AHR---------TGG----ME----338 398 750 650 678 735 8 % B à 8

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T13825 T13826 T13826 C;Species: Drosophila melanogaster C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 17-Nov-2000 C;Accession: T13825 R;Haysshi, S:; Rubinfeld, B.; Souza, B.; Polakis, P.; Wieschaus, E.; Levine, A.J. Proc. Natl. Acad. Sci. U.S.A. 94, 242-247, 1997 A;Title: A Drosophila homolog of the tumor suppressor gene adenomatous polyposis coli

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770	1110 SETNRVGSNHGINQNVSQSLCQEDDYEDDKPTNYSERXSEEEQHEEEERPTNYSIKYNEE 1169	779	1170 KRHVDQPIDYSLKYATDIP-SSQKQSFSFSKSSGQSSKTEHMSSSSENTSTPSS 1223	812 KSTITPPAETVPEKSEGQEILLILDDSVKCYQTEDTPYVISNAASVTDLRVAA 864	1224 NAKRQNQLHPSSAQSRSGOPQKAATCKVSSINQETIOTYCVEDTPICFSRCSSLS 1278	865 KADREABVREVTEVTSKEGAPKKLPKLSQCGSGSYTPEKPINYCEBGTPGYPSRYDSLS 924	1279 SLSSABDRIG-CNOTTQEADSANTLQIARIKGKIGTRSAEDPVSEVPAVSQHPRTKSSRL 1337	925 SLDESGKANQAIVGTDADIKPKLEKQEEQE 954	1338 QGSSLSSESARHKAVEFPSGAKSPSKSGAQTPKSPPEHYVQFTF11111111111111111111111111111111111		1398 SRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQTAQTKREV 1452	993 DVDVANCDDKSSVVSD-FSRLASGVISPSEIPDSPTQSMPQS1033	1453 PKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSSLSALSLD 1512	1034 PRRNSVAGSGQNVDSPPVVIPASLQPLRSVFE-DDLSSFNVEHTPAQFSTATSLSNLSI- 1091	1513 EPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKE-AEKTID 1558	1092VDDEKAPAVWTEDNEBLLLANCINMGMQRKPTEAVKSTVVNSEVDVAEETIR 1144		1145 SYCTEDTPALLSKVPSNTNLSVISMSSTDPKDATAGQAQMYAHQLSDDVSSNASDCGGAS 1204	KLLPSQNRLQPQKHV	1205 GHLLQQCIRDGMKKPLGEATSDPIAMLRRGGNELPGYLPS 1244		1245ADEMNK-FLVEDSPCNFSVVSGLSNLTVGSSLVGPAVQLKETE-PSSADQNPEMKR 1298	1687 RDIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAEC	1299 SLANRSKSRRPPHWÖDDSLSSLSIDSEDDTNLLSQAİAACCNRPKSNLGFSSNGKRSSSL 1358	1728INSAMPKGKSHKPFRVKKIMDQVQQASASSSAPNKNQLDGKK 1769	1359 SSSQPIAİNAATSASSLNSAMTVRKSQQQESYSSVDSSDSNDNQSKSLFELCILKGMYKT 1418	1770 KKPTSPVKPIPQNTEYRIRVRKNADSKNNINAER 1803	1419 KEPGARAQOMQEQPIVGSSSVQSNPSLKQFDSLPVQLPSSGQVKKQKHHHHHHHHRRERER 1478	1804 VFSDNKDSK-KONLKNNSKDFNDKLPNNBDRVRGSFAFDSPHHYTPIEGTPYCFSRND 1860	1479ERKDEKLLQECINTGISKKIN-AVPKNVLATSAAALEPCHPMAATT 1523	SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQA-TAKQPI- 1	SASALSTAAPDVEQKAHATSNPQQQSSTHPSSHILPNPIDAIATVTDTARSPAA	1919 -NRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCF 1963  1919 -NRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCF 1963  1919 -NRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCF 1963	CHARLE THE THE TABLE TO A CONTROL TO A CONTROL TO A CONTROL THE TABLE THE TA	1964
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ව ර	2109	NSIVSSIHQAAAAACLSRQASSDSDSILSLKSGI-SLGSPFHLTP 2152
& <del>8</del>	2153	DQEBKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQ 2212
රු සි	2213	MKQPLQANMPSISRGRIMIHIPGVRNSSSTSPVSKKGPPL
දු දු	2254	KIPASKSPSEGQTATISPRGAKPSVKSELSPVAR 2287  EDEDATMUDYSSAESTPKHGSTPSPNRRSLTPKDKRRLTKDRFKTYTIATSCEMEAPEAN 2017
දු ද	22.88	QTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPI2321
8 8	3 2	OSP-GRNSISBGRNS18PPNKLS 234
ΩÞ	2078	AMMQQFTFITDINIGHSQETCESTDHPEDAGESPECDQNSFTESCDGGEPDHLPPPPSIV 2137
\$ 6 6	2344	OLPRISSPSTASTKSSGSGKWSYTSPGROMSOONLTKQTGLSKNASBIPRSESA 2397 
<u>ک</u> م	2398	SKGLNOMNNGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQSTF,2443
ò	2444	APSPTLRRKLEESAŠFESLSPSSRPASPTRGQAQTPVLSPSLPDMSLSTHS
අධ	2231	
λ	2504	IEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVST 256
qq	2259	arrmtporantslrlaa 230
y d	2564	WRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFS 2621 :
λŏ	2622	PINSTSQTVSSGATNGABSKTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTCN 2678
DP	2364	SSSNLRTQKTKSSNMLNANGTKPTLLRSSTFDN 2397
Qy	2679	TPPVIDSVSEK 2689
q	2398	TPSTAGGVKSK 2408
RESULT 5 T13564 microtubule N,Alternate C,Date: 13-C,Accession R,Spanos, I submitted t A,Descripti	bubule-as ubule-as ies: Dra : 13-Aug ssion: Cos, L.; ted to t ted to t rription	le-associated protein homolog - fruit fly (Drosophila melanogaster) te names: hypothetical protein EG:49E4.1 3-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000 on: T13564 L.; Papagiannakis, G.; Siden-Kiamos, I.; Louis, C. to the EMBL Data Library, April 1999 tion: Sequencing the distal X chromosome of Drosophila melanogaster. ce number: 217689

A, Riscues; paril minary, translated from GB/ENGL/DDBJ A, A, Sistuene; paril minary, translated from GB/ENGL/DDBJ A, A, Sistuene; paril minary, translated from GB/ENGL/DDBJ A, MASSIACE CHEERS RELLA.031128; p1DN:CAA20006.1. A, COSSETERIZATION RELLANDING PROPERTY. 1669/3; 2566/1; 4798/3; 2572/1 A, INTOCOSE A, A, A, A, B, SOCIA 618-5; DB 2; Length 5327; A, MANOCES; DS; SBG4, 12/3; 1704/3; 1797; 1272/1; 1669/3; 2566/1; 4798/3; 2572/1 A, MARSIAL SANDOLLOVDAIDANBRANGES-IDANBRANKENIZOGGS: 55 91 AREXIDALIANDANDARENIALEGE-BARGES-IDANBRANKENIZOGGS: 55 91 AREXIDALIANDARENIALEGE-BARGES-BARGES-IDANBRANKENIZOGGS: 55 91 AREXIDALIANDARENIALEGE-BARGES-
13564 1.minary; translated from GB/EWBL/DDBJ 5.927 5.927 5.104/3; 179/1; 232/1; 166/3; 2566/1; 47 6.1500 6.25/3; 104/3; 179/1; 232/1; 166/3; 2566/1; 47 6.1500 6.25/3; 104/3; 179/1; 232/1; 166/3; 2566/1; 47 6.1500 6.25/3; 104/3; 179/1; 232/1; 166/3; 2566/1; 47 6.1500 6.25/3; 104/3; 179/1; 232/1; 166/3; 2566/1; 47 6.1500 6.25/3; 104/3; 179/1; 232/1; 166/3; 2566/1; 47 6.25/3; 104/3; 179/1; 232/1; 166/3; 2566/1; 47 6.25/3; 104/3; 179/1; 232/1; 166/3; 2566/1; 47 6.25/3; 104/3; 179/1; 232/1; 166/3; 2566/1; 47 6.25/3; 104/3; 179/1; 232/1; 166/3; 2566/1; 47 6.25/3; 104/3; 179/1; 232/1; 166/3; 166/3; 2566/1; 47 6.25/3; 104/3; 179/1; 232/1; 166/3;

q	1567 AESAKPPIEFREVSRPESVI	SVIDGIKDESAKPESRRDSPLASKE 1608
à	836 SSRGSLDSSRSEKDR	-GSLDSSRSEKDRSLERERGIGLGNYHPATENPGISSKRGLQISTTAAQIA 888
qq	1609 ASRPESVLESVKDEPIK	ASRPESVLESVKDEPIKSTEKSRESVAESFKADSTKDEKSPLTSKDISRPESAVE 1664
à	889 KVMEEVSAIHTSOEDRS	KVMEEVSAIHTSQEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCS 948
qq	1665 NVM-DAPFKETSRPESA	.VGSMXDESMSKEPSRRESVKDGAAQSRETS 1710
à	949 MPYAKLEYKRSSNDSLN	MPYAKLEYKRSSNDSLNSVSSNDGYGKRGOMKPSIESYSEDDESKFCSYGOYPADLA 1005
qq	1711 RPASVAESAKDGADDLK	RPASVAESAKDGADDLKELSRPESTTQSKEAGSIKDEKSPLASEEASRPASVAESVKDEA 1770
λζ	1006 HKIHSANHMDD	-NDGELDTPINYSLKYSDEQLNSGRQSPSQNERW 1049
QD	1771 EKSKEESRRESVAEKSP	EKSKEESRRESVAEKSPLPSKEASRPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEA 1830
λά	1050 ARPKHIIEDEIKQS	ARPKHIIEDEIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQ 1095
<b>q</b> 0	1831 SRPASVAESIKDEAEKS	KEESRRESVAEKSPLPSKEASRPASVAESIKDEAEKSKEE-SR 1889
λά	1096 QECVSPYRSR	SPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKPINYSE 1145
q <sub>C</sub>	1890 RESVAEKSPLPSKEASR	RESVAEKSPLPSKEASRPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEASRPASVAE 1949
λζ	1146 RYSEB-BOHBEBERPIN	YSLK
qC	. 1950 SIKDEAEKSKEESRRES	SIKDEAEKSKEESRRESVAEKSPLPSKEASRPASVAESIKDEAEKSKEESRR 2001
λζ	1205 SSKTEHMSSSSENTSTPSSNA-	SSNAKRONOLHPSSAOSRSGOPOKAATCKVS 1252
qc	2002 ESVAEKSPLPSKEASRP	ESVAEKSPLPSKEASRPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEASRPASVAES 2061
λζ	1253SINOFTIQIYC	SINQETIQTYCVEDTPICFSRCSSLSSLS-SAEDFIGCNQTTQEADS-ANTLQ1 1304
)p,	: : : : : : : : : : : : : : : : : : :	IKDEAEKSKEESRRESAAEKSPLPSKEASRPASVAESVKDEADKSKEESRRESMAESGKA 2121
ž	1305 AEIKGKIGTR	ᅂ
qc	2122 QSIKGDQSPLKEVSRPE	QSIKGDQSPLKEVSRPESVAESVKDDPVKSKEPSRRESVAGSVTADSARDD 2172
à	1358 AKSPSKS-GAQTPKSPP	AKSPSKS-GAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFESRSIASSVQSEPCSGMVSG 1416
q	2173 -QSPLESKGASRPESVV	DSVKDEAEKQESRRESKTES 2208
<i>ኢ</i>	1417 IISPSDLPD-SPGQTMP	IISPSDLPD-SPGQTMPP-SRSKTPPPPPQTAQTKREVPKN-KAP 1458
q	2209 VIPPKAKDDKSPKEVLQ	
λ.	1459 TAEKRESGPKQAAVN	TAEKRESGPKQAAVNAAVQRVQVLPDADILLHFAIESTPDGFSCSSSLS 1507
q	2269 LASKEASRPGSVAESIK	YDLDKPQIIKDDKSTEHSRRESLEDKSAVTSEKSVSRPLSVAS 2328
Ä	1508	1512 
q	2329 DHEAAVAIEDDAKSSIS	PKDKSRPGFVAETVSSPIEEATMEFSKIEVVEKSSLALSLQGG 2388
λ;	1513	
q	2389 SGGKLQTDSSPVDVAEG	SGGKLQTDSSPVDVAEGDPSHAVASVSTVTPTLTKPAELAQIGAAKTVSSPLDEALRTPS 2448
λ	1528 VQENDNGNETESEQPKE	VOSNDNGNETESEQPKESNENQEKEAEKTIDSEXDLLDDSDDDIEILEECIISAMPTKS 1587
ą	2449 APEHISRADSPAECASE	
λ;	1588 SRKGKKPAQTASKLPPPVARKPSQLPVYKL-	VARKPSQLPVYKLLPSQNRLQPQKHVSF 1632
q	2509 STEISRPASAGETASSP	STEISRPASAGETASSPIEEAPKDFAEFEQAEKAVLPLTIELKGNLPTLSSPVDVAHASV 2568
≵	1633 TPGDDMPRVYCVE	DMPRVYCVECTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQSGEFEKRD 1688
ą	2569 QPAELSKVDIEKTA	OPAELSKVDIEKTASSPIDEAPKSLIGSPAEERPESPAESAKDAAESVEKSKDA 2622

\(\delta \) \(\de	Reverse Branch and Control	8     8 <th>4 6 4 6 4 </th>	4 6 4 6 4 
1689 TIPTEGRSTDEAQGGKTSSVTIPELDDNKAEE	1872 VDLSR	2150 UTPDQEEKPETSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEI 2209 3159DBABKSKEESRRESVABKSPLPSKEASRPASVAESVKDEADKSKEESRRE- 2210 SGQMKQPLQANMPSISRGRTMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGQT 2266 3209 SGAEKSPLASKESPARATO	GGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSS GGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSRESVAEKSPLASKEASRPAGVAESVKDEAEKSKEESRRESVAEKS SLPRVSTWRRTGSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRK
8 8 8 8 8 8			2 4 6 6

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hypothetical protein SA2447 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
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C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Accession: P90073
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch
R;Kuroda, M.; Ohta, T.; Hochyama, I.; Baba, T.; Tnoue, R.; Kaito, C.; Sekimizu, K.; E.
C; Sinba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
Lancet 357, 1225-1240, 2001
Lancet 357, 1225-1240, 2001
A;Feference number: A89758; MuID:21311952; PMID:11418146
                                                                                                                                                                                            3625 SKEASR-PIS----VAESVKDEADKSKEESR-------RESGAEKSPLASME 3664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       982 SIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGELDTPINYSL---KYSDEQLNS 1038
                                               2728 VDAPDQKGTEIKPGQNNPVPVSETNESPIVERTPFSSSSSKHSSPSGTVAARVTPFNYN 2787
                                                                                                                                                                                                                                                                                                                                          3665 ASRPISVAESVK--DETEKSKEESRRESVIEKSPLPSKEASRPISVAESVKDEAEK-SKE 3721
2615 IXEN-----EPSPINSTSQTVSSGAINGAESKTLIYQMAPAVSKTEDVWVRIEDCPIN 2667
                                                                                                                                                     2668 NPRSGRSPIGNTPPVIDSVSEKANPNIKDSKDNOAKONVGNGSVPMRTVGLENRLISFIQ 2727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary
;Molecule type: DNA
;Residues: 1-2271 «KUR»
;Cross-references: GB:BA000018; PID:g13702612; PIDN:BAB43752.1; GSPDB:GN00149
;Experimental source: strain N315
;Genetics: SA2447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               809 NRSDNFNTGNMTV-LSPYLNTTVLPSSSSSRGSLDSSRSEKDRSLERERGIGLG-NYHPA 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  606 ICAVDGALAFLVGTLTYRSQTWTLAIIE-----SGGGIL------RNVSSLI 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      647 ATNEDHRQILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSM 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413 ADNAAKLNVQPTNNTFQDFDINYNGDTKVMTVKYAĞQTW----TRNISD----W----IAK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462 SGTINFSLSMTASTGGATNLQQQQFGTFEYTESAVTQVRYVDVTTGKDIIPPKTYSGNVD 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     754 V-----RKOKALEAELDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYVFDTNRHDD 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      707 LKNLIHSKHKMIAMGSAAALRNLM-----ANRPAKYKDA----NIMSPGSSLPSLH 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --RSSAAHTHSNITYNFTKSENSNRTCSMPYAKLEYKRSSNDSLNSVSSNDGYGKRGQMKP 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | : | : | : | 353 IGGLSNAFGFKLDTYHNTSKPNSAAKANADPSNVAGGGAFGAFVTTDSYGVATTYTSSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                671 GDQSSBVYSPISPIKIATQDNSGNAVTNTVTGLPSGLTFDSTNNTISGT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.6%; Score 518; DB 2; Length 2271; Best Local Similarity 19.5%; Pred. No. 1.8e-13; Matches 452; Conservative 333; Mismatches 1000; Indels 534; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3722 BSRRESVAEKSPLASKESSRPASVAESIKDEAEGIKQESRRESMPESG 3769
                                                                                                                                                                                                                                                                                                                                                                                                                                                2788 PSPRKSSADST----SARPSQIPTPVNNNTK--KRDSKTDSTESSG 2827
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	1099 VSPYRSRGANGSETNRVGSNHGINQNVSQSLQQEDDYBDDKPTNYSERYSEEEQHEEEER	oá L	1158 863	QV Db
	1159 PTNYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSKSSGQSSKTEHMSSSSBNT		1218 904	oy Dp
	1219 STPSSNAKRQNQLHPSSAQSRSGQPQKAATCKVSSINQETIQTYCVEDTPICFSRCSS		1276 954	P Q
	1277 LSSLSSAEDEIGCNQTTQEADSANTLQIAEIKGKIGTRSAEDPVSEVPAV		1326 1011	දු පු දු
	1327 SQHPRTKSSRLQGSSLSSESARHKAVEPPSGAKSP8KSGAQ-TPKSPPEHYVQETPLMFS    1		1385 1070	, B (
	1386 RCTSV8SLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPPP		1442 1126	à qa
	1443 PQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSC		1502	6 6 6
	1503 SSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEA		1553 1226	A G
	1554 EKTIDSEKDLLDDSDDDDIEILEECIISAMPTKSSRKGKKFAQTASKLPPPVAR-KPSQL :		1612 1279	ර් සි ර
	1613 PVYKLLPSQNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAG 1280 STSLSMSTSTSLSNSTSLSTSLSDSTSDSKSDSLSTSMSTSDSISTSKSDSISTS		1672 1334	À
;	1673 EGVRGGAQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAE  1335 TSLSGSTSESESDSTSSSESKSDSTSMSISMSQSTSGSTSTSLSDSTSTSLSLSAS		1726 1394	දු පු
	1727 CINSAMPKGKSHKPFRVKKINDQVQQASASSSAPNKNQLDGKKKKPTSPVKPIPQNTEYR		1786 1426	충 셤
	1787 TRVRKNADSKNNLNAERVFSDNKDSKKQNLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHY  1427 TYTSQSTSQSESTSTSTSLSBSTSISKSTSQSGSTSTSASLSGSESESDSQSISTSASES		1846 1486	RES T34 hyp
	1847 TPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQOS		1906 1538	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	1907 ANKTQAIAKQPINRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIBNTPVCFSHN		1966 1578	8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
	1967 SSLS-SLSDIDQENNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDT-PVCFSRN		2024 1628	A A A A
	2025 SSLSSLSIDSEDDLLQECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQ 	0 ⊷	2084 1658	# 0 0 £ #

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                                                                                                                        1659 --DSVSDSTSDSTS----ASTSGSMSVSISLSD-----STSTSTSASBVMS--ASISD 1703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2737 EIKPGQNNPVPVSETNESPIVERTPFSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSAD 2796
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2085 RPDSEHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2202 KVRSNSEISGQMKQPLQANMPSISRGRTMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1746 SLRKSESVS-----ESSSLSGSQSM--SDSVSTSDSSSLSVSTS---LRSSESVSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2322 QSPGRNSIS-PGRNGISPPNKLSQLPRISSPSTASTKSSGSGKMSYTSPGRQMSQQNLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2381 QTGLSKNASSIPRSESASKGLNOMNNGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2560 RVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENE
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                                                                                                                                                                                                                                                                                      GSPFHLTPDQEEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKS---LITG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2620 FSPINSTSQTVS---SGATNGAESKTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2677 GNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNGSVPMRTVGLENRLTSFIQVDAPDQKGT
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Potherical protein K06A9.1a - Caenorhabditis elegans
Species: Caenorhabditis elegans
Species: Caenorhabditis elegans
Species: Caenorhabditis elegans
Species: Caenorhabditis elegans
Accession: T34434
Geisel, C.; Gattung, S.
Inhary, December 1996
Description: The sequence of C. elegans cosmid K06A9.
Reference number: 221525

Accession: T34434
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
Molecule type: DNA
Sesidues: 1-222 <GEI>
Cross-references: EMBL:U80846; PIDN:AAC70890.1; GSPDB:GN00028; CESP:K06A9.1a
Experimental source: strain Bristol N2; clone K06A9
Genetics: Genetics:

A,Map position: X A,Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1; 2075/?

SPVARQTSQIGGSSK 2297 | : :| | | :: STLL--SSTISGSTQ 1444 ----AQTPVLSPSLP 2489 : | :: | TVASSTTGLVSTSTV 1681 SPSRLPINRSGTWKR 2549
: | : | | |
TGSTVTMGSSSTSGV 1727 NSISGTKOSKENOVS 2607 :: | | | : | | STSSGTVGSTMSQSS 1787 ----ATNGAESKTLI 2644 :| | : TVASSTAGLVSTSTV 1837 SGVSTSSASSTQPOM 1895 PVPVSET-NESPIVE 2758 | | :|| SGTVGSTISESSTAA 1946 RPSQIPTPVNNNTKK 2815 NKLSQ-----LP 2346 SIPRSESASKGLN-- 2402 :: | :: | :: | TVTMGSSSTSGVSTS 1564 SGTVGSTISESST-T 1623 ANPNIKDSKDNQAKQ 2704 SGSSTPTPNPSÖSTS 1284 SSEASTSGSSFKTSP 1344 SISRGRIMIHIPGVR 2237 ST-----VPSST 1396 MSTŠQGSSAGSTVAS 1504 DRSERPVLVRQSTFI 2444 ------PDQEEK 2157 SESKGIKĢG---- 2191 lange 29-Oct-1999 ยน

	QY         1228 QNQLHPSSAQSRSGQPQKAATCKVSSINQETIQTYCVEDTPICFS	RESULT 9 T23330 hypothetical protein K04G2.8b - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T2330 R;Gardener, A. submitted to the EMBL Data Library, July 1996 A;Reference number: Z19727 A;Reference number: Z19727 A;Reference number: Z19727 A;Reference number: Z19727 A;Reference number: Z19727 A;Reference number: Z19727 A;Reference number: Z19727 A;Reference number: Z19727 A;Residues: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-1188 <wilb- 1="" 1-1188="" 1069="" 113="" 1163="" 2;="" 355="" 3;="" 3<="" 551="" 61="" <wilb-="" a;cross-references:="" a;gene:="" a;introns:="" a;map="" a;reperimental="" a;residues:="" c;genetics:="" cesp:k04g2.8b="" clone="" embl:z75712;="" gspdb:gn00019;="" k04g2="" pidn:cab00048.1;="" position:="" source:="" th=""><th>  Query Match   3.5%; Score 514.5; DB 2; Length 1188; Best Local Similarity   21.9%; Pred: No. 1.1e-13; Matches 289; Conservative 216; Mismatches 564; Indels 249; Gaps 52; Matches 289; Conservative 216; Mismatches 564; Indels 249; Gaps 52; Qy   271 MATSONGGGSTTRMDHETASVLSSSTHSAPRRLITSHLGTKVENVYSLISMLGTHDKDDM 330   1                                  </th></wilb->	Query Match   3.5%; Score 514.5; DB 2; Length 1188; Best Local Similarity   21.9%; Pred: No. 1.1e-13; Matches 289; Conservative 216; Mismatches 564; Indels 249; Gaps 52; Matches 289; Conservative 216; Mismatches 564; Indels 249; Gaps 52; Qy   271 MATSONGGGSTTRMDHETASVLSSSTHSAPRRLITSHLGTKVENVYSLISMLGTHDKDDM 330   1
A:Wolecule type: DNA A;Residues: 1-1186 <wll> A;Cross-references: EMBL:Z75712; PIDN:CAB00045.1; GSPDB:GN00019; CESP:K04G2.8a A;Experimental source: clone K04G2 A;Experimental source: clone K04G2 Cell 90, 707-716, 1997 A;Title: Wnt signaling and an APC related gene specify endoderm in early C. elegans embrackersence number: 215051; MUID:97433081; PMID:9288750 A;Accession: T03822 A;Accession: T03822 A;Accession: RNA A;Residues: 1-1186 <roc> A;Accession: RNA A;Residues: 1-1186 <roc> A;Cross-references: EMBL:AF013950; NID:g2338717; PIDN:AAC47747.1; PID:g2338718 A;Experimental source: strain Bristol C;Genetics: apr-1; CESP:K04G2.8a A;Map position: 1 A;Note: apr-1 A;Note: apr-1 A;Note: apr-1 A;Note: apr-1</roc></roc></wll>	Query Match  2.5%; Score 516.5; DB 2; Length 1186;  Best Local Similarity 21.9%; Pred. No. 9.1e-14;  Matches 289; Conservative 216; Mismatches 562; Indels 251; Gaps 52;  QY 271 MATSGNGGGSTTRMDHETASVLSSSTHSAPRILTSHLGTKVENVYSLLSMLGTHDKDDM 330  Db 1 MSSSSDENETTIHRTGSNTGGSGIXSQPRAGSSKRTSNVRHDVSDVDDE 50  QY 331 SRTLLAMSSSQDSCISMRQSGCLPLIQLLHGNDKDSVLLGNSRGSKEARARASAALHN-389  E EHYARFREDTAIEVDDAITVLLSQIRFRDIVVPTDEDDNKLRELHEK 100  QY 390IHRQPDDKRGRREIRVLHLLEQIRAYCETCWEWQEAHEPGMDQDKNPMPAPVEHQI 446  DD 101 IFALITSESDVRKRRLKALPASNCKREQVYYLRRKPSTHRRANGMA 504  447 CPAVCVLMKLEPDEBHRHAMNELGQLAIAELLQUDCHNYGINFILLRRYAGMA 504  150 NAALHTIVKESFGEEYRKVATVLGLVVBALABVLILEWHTFGINFTNIRKLIANA 209	OY 505 LTRUITEGDVANKATLCSWKGCKRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLR 564  Db 210 LTRLITYGQIHSKRRLCSYDGFIRCVV-RIVIESPNITQVYAGLIRNLSWNADSGMSEALQ 268  OY 565 EVGSVKALMECALEVKKES-TLKSVLSALWNLSAHCTENKADICAVDGALAFLVGTLTYR 623  :	QY  802 DTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSSRGSLDSSRSEK-DRSLERERG 857  1

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us norvegicus (Norway rat)

1993 #sequence_revision 31-Dec-1993 #text_change 13-Aug-1999

31359; S22108

Hammarback, J.A.; Muller, R.; Vallee, R.B.; Garner, C.C.

267, 16561-16566, 1992

hule-associated proteins 1A and LC2. Two proteins encoded in one messenge

369: A43359; MUID:92355629; PMID:1379599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133;
----DSIENQTRDDTIYVNAPVVEAEQERIYMNALKQQK 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRHDDNRSDNF-----LPSSSSSR 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GSLDSSR----SEKDRSLE-----RERGIGLG----NYHPATENPGTSSKR 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EDHRQILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWD 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              801
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                                                                                     PDSP--GQTMPPSRSKTPPP----PPQTAQTKREVPKNKAPTAEKRESGPKQAAV 1472
                                                                                                                                             AVSM--LKNLIHSKHKMIAMGSAAALRNLMANRPAKYKD--ANIMSPGSSLPSLHV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----RKOKALEAELDAQHLSETFDNIDNLSPKASHRSKQR----HKQSLYGDYVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.3%; Score 477; DB 2; Length 2774;
ilarity 18.7%; Pred. No. 1.2e-11;
Conservative 359; Mismatches 1039; Indels 958; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mENA
74 <LANN:
es: 8180196; NID:9205537; PIDN:AAB48069.1; PID:9205538
extracted from NCBI backbone (NCBIN:111039, NCBIP:111040)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ource: strain Sprague Dawley icrotubule-associated protein MAP1B otubule binding; phosphoprotein
         KOKHYPEE--
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442 DAKKDEKRKOTKPEVKKLSKPDLKPFTPEVRKTLYKAKAPGRVKVDKGRA 491	1029 LKYSDEQLNSGRQSPSQNE		DSGAEVEKETWEERKQREAELGPENTAAREESEAKVKEDVIEKAELEEMETHYSDE DSGAEVEKETWEERKQREAELGPENTAAREESEAKVKEDVIEKAELEEMETHYSDEE		ENTSTPSSNAKRQNOLH		1305 AEIKGKIGTRSAED-PVSEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFPS-GA 1358   :		1405VQSEPCSGMVSGIISPSDLPDSPGQTMPPS	1442PPQTAQTKREVPKNKAPTABKRE	1471AVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSSLSA 1508	1509 LSLDEPFIQKDVELRIMPPVQENDNGHITSSEQP 1542	1543 KESNENQEKEAEKTIDSEKDLLDDSDDDDIEILEECIISAMPTKSSRKCKKPACTAS 1599 1162 CSLKEQQPHKDLWPMVSPEDTQSLSF8EESPSKETSLDISS 1202	1600 KLPPPVARKPSQLPVYKLLPSQNRLQPQKHVSFTPGDD 1637 	1638 MPGE 1673 :	1674 GVRGGAQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPE 1712		183
임	유 상	<u>ک</u> ۾	Sy dy	<u>ک</u> ۾	S G	b Sy	<u>&amp;</u> 8	g 2	\(\delta \)	& 8	& 8	<u>ک</u> ۾	<b>≵</b> 4	<u>સ</u> ક	≿ છ	<u></u> કુ	<u>≯</u> &	≿:

Š	1833 RVRGSFAFDSPHHYTPIEGTPYCFSRNDSLSSLDFUDDUDLSREKAELRKAKE-	1889NKE 1889
. A	1473 RAPEHSIP	ALGKE 152
à	1890 SEAKVTSHT	ILOKOSTFPOSSKDIPDRGAA 1946
ą	1522	:::    ::    : :  FVEDKTTTSKETVLDQKSAEKA 1572
à.	1947 -	-KENEPIKETEPPDSQGEP 1999
ą	1573 DSVEQODGAALEKTRALGLEESPAEGSKAREGEKKYWKEQDVVQGWRETSP-	WKEQDVVQGWRETSPTRGEPVG 1630
<u>خ</u>	2000SKPQASGYAPKSFHVEDTPVCFSRNSSLSS	FHVEDTPVCFSRNSSLSSLSIDSEDDLLQECI-SSAMPKK 2050
ą	1631 GQKEPVPAWEGKSPEQEVRYWRDRDITLQQDAYWRELSCDRKVWFPHELDGQGARPRYCE	: : : : LSCDRKVWFPHELDGQGARPRYCE 1690
Z	2051 KKPSRLKGDNEKHSPRNMGGILGEDLTL	-KHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFDWK 2102
ą	1691 BRESTFLDEGEDETTPLQHTPRSPWTS	PWISDFKDFGEPLPQKGLEVERWL 1739
<b>~</b>	2103 AIQEGANSIVSSLHQAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEK	KSGISLGSPFHLTPDQEEKP 2158
ą	1740 A	
⋩		TLETKKIESESK 2186
ą.	1759 FEIISPPASPPEMTGQRVPSAPGQESPVPDTEST	::  APGQESPVPDTESTAPWRNEPTTPSWLAEIPPWVPKDR 1816
<b>≿</b> :	2187GIKGGKKVYKSL	-GIKGGKKVYKSLITGKVRSNSEISGOMKOPLOANMP 2222
ą	1817 PLPPAPLSPAPAPPTPAPEPHTPVPFSWGLAEYDSVVAAVQEGAAELEGGPYSPLGKDYR	: VAAVQEGAAELEGGPYSPLGKDYR 1876
<b>~</b>	2223 SISRGRTMIHIPGVRNSSSSTSPVSKKGPPLKT	PASKSPSE 2263
ą	1877 KAEGEREGEGGAGAPDSSSFSPKVPEAGESLATRDTEQTEPEQREPTPYPDERSFQYAD	:  : SQTEPEQREPTPYPDERSFQYADI 1936
≿ı	2264GQTATTSPRGAKPSVKSELSP	PSVKSELSPVARQTSQIGGSSKAPSRSGSRDST 2308
ð	1937 YEQMMLTGLGPACPTREPPLGASGDWPPHLSTKEEAAGCNTSAEKETSSPASPQNLQSDT	AGCNTSAEKETSSPASPONLOSDT 1996
<b>≱</b> .	2309 PSRPAQQPLSRPIQSPGRNSISPG	RNGISPPNKLSOLPRT 2348
۵	1997 PAFSYASLAGPAVPPRQEPDPGPNVEPSITPPAV	DPGPNVEPSITPPAVPPRAPISLSKDLSPPLNGSTVSCS 2054
<u>⊀</u>	2349 SSPSTASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKNASSIPRSESASKGLNO-	SKNASSIPRSESASKGLNOMN 2405
Q	2055 PDRRTPSPKETGRGHWDDGTNDSDL	
<u>~</u>	2406 NGNGANKKVELSRMSSTKSSGS	2427
۵	2104 HSSLWPETEAYSSLSSDSHLGSVRPSLDFPASAFGFSSLQPAPPQLPSPAEPRSAPCGSL	SSLQPAPPQLPSPAEPRSAPCGSL 2163
<b>&gt;</b>	2428ESDRSERPVLVRQSTFIKEAPSPTLRRKLEESASFES	ESSASFESLSPSSRPASP- 2474
д	2164 AFSGDRALALVPGTPTRTRHDEYLEVTKAPSLDSSLPQLPSPSSPGGPLLSNLPRPASPA	:
۸	2475TRSQAQTPVLSPSLPDMSLSTHSSVQAGG-	3WRKLPPNLSPTIEY 2517
д	2224 LSEGSSSEATTPVISSVAERFPPGLEAAEQSAEGLGSGKESAAHSLWDLTP-	GKESAAHSLWDLTPLSPA 2278
>-	2518 NDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLP	ISSSLPRVSTWRR 2566
Ω	2279PSASLDLAPAPAPAPAP	GLPGDLGDGTLPCRPECTGEL 2318
>-	2567 TGSSSSILSASSESSEKAKSEDEKHVNSISGTK	ISGTKQSKENQVSAKGTWRKIKENEF 2620
۵	2319 TKKPSPFLSPSGDHEANGPGETSLNPPGFVTATAEKEEAEAPHAWERGSWPEGAERSS	KEEAEAPHAWERGSWPEGAERSS 2376
>-	2621 SPTNSTSQTVSSGATNGAESKTLIYQM	APAVSKT 2654
Ω	2377 RPDTLLSSEQPIRPGKSSGGPPCSLSSEVEAGPQGCATDPRPHCGELSPSFLNPPLPPST	TDPRPHCGELSPSFLNPPLPPST 2436

1021 PKTGDKNPDITTDGEDSTSETSGGEGGPKGKSKGQPPGDKGSEVKKPTSEVDGPGNLSGT 1080 1397 ESRSIASSVQSEPCSGWVSGIISPSDLPDSPGOTMPPSRS 1436 1397 KGKSNVPLKPTDLPEEGSGILTTSSGGKNSTFEHGTKLERLPP 1123 1437 KTPPPPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFAT 1493 1124 KTEDKSSETPQLGLEISAGKKPPEPGGTSKEVG	1172 DSDSVGLEISGSDLTKATKKPHVEIEGSGTGDEBITATTRDVSKSTKKFRVEVDGGDNGE 1231 1537TESEQPKESNENQEKEAEKTIDSEKDLLDDSDDDDIBILEECIIS 1581 1232 TSGVDGKPTTPAPTPSSSAESSTSRIPTTSEASPEGGSGEAGVPESPDGSGESSTSAPDG 1291 1582 AMPTKSSRKGKKPACTASKLPPPVARKPSQLPVYKLLPSGNRLQPQKHVSFTP 1634 1292 VSPTSSATAPBVTTSAGSTPDAVEESGIPSTSARPEPETTAPSTEVTSPEGSGTE 1349					1917 NTIGSFNCVCLEGFKKVDEKCVVDEKKQPNREKTEIBENSSSSNSGQEKPTTKGIVSST 1976 2075 DLTLDLKDIQRPDSEHGLSPDSENFOWATQEGANSIVSSLHQAAAACLSRQASSDSDS 2134 2075 SATSSESTTAEPHVTTSISSTTSTKDMTSSKSPENVTMSSESPEVSTSSSKSTTASET 2034 2135 ILSLKSGISLGSPFHLTPDCEEKPPTSNKGPRILKFGEKSTLETKKIESESKGI 2188 2035 IVSSTPSESSSSEAPLTSSPATTTEVITESSSVKSTTPKEESSSE 2078
4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	8 6 8 6 8	8 6 8 6 8 6	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6 6 6 6	42 42 42
Qy 2655 EDVWVRIEDCPINNPRSGR-SPTGNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNG 2709  1	Oy 2800ARPSOIPTPVNNNTKK 2815  Db 2614 TVPRPRSTPSQVTSAEEK 2631  RESULT 11 T34513  hypothetical protein ZK783.1 - Caenorhabditis elegans	Cipate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 Cipate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 Cipate: 29-Oct-1999 #sequence revision 29-Oct-1999 #text_change 29-Oct-1999 Cipate: 29-Oct-1999 #sequence of cip	. ""	**HITEDEIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPHFG 	IRVRITTLGEDGEPETATKPGISAPDKTGEGSKTE SQQSSKTEHMSSSSENTSTPSSNAKRQNQLHPSSA   : : :	Qy 1288

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1093
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Publication protein F07All.6b - Caenorhabditis elegans
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Rubmitted to the EMBL Data Library, October 1995
A;Recession: T20532
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: T2772
A;Rosiduss: 1-272 \*MIL>
A;Cross-references: EMBL:Z66511; PIDN:CAB54211.1; GSPDB:GN00020; CESP:F07A11.6b
A;Experimental source: clone F07A11
A;Residuse: 1-272 \*MIL>
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A;Residuse: EDDESKFCSYGGYPADLAHKIHSANHMDDNDGEL-----DTPINYSLKYSDEQLNSGRQS 1042 2085 T----SASASASTS------ASASASTSASASASASTSASESASTSASASTS 2126 2025 ESASTSASASASTSASASASASASASTSASASASASTSASASASASASTSASASAS 2084 2762 PSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVNNNTKKRDSKTD 2821 2582 EKAKSEDEKHVNSISGTKOSKENQVSAKGTWRKIKENEFSPTNSTSQTVSSGATNGAESK 2641 2642 TLIYOMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDNQ 2701 2522 PAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSESS 2581 395 --SSSRDRQNLHDPLQTRSSVEH----HTNQEDQENNASGSDS----SSDSDSEEGSSS 443 928 AHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSSNDSLNSVSSNDGYGKRGQMKPSIESYS 987 871 GTSSKRGLQISTTAAQIAKVWEEVSAIHTSQEDR---SSGSTTELHCVTDERNALRRSSA 2702 AKQNVGNGSVPMRTVGLENRLISFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVERTP Query Match 2.9%; Score 428.5; DB 2; Length 2722; Best Local Similarity 18.6%; Pred. No. 1.1e-09; Matches 460; Conservative 324; Mismatches 893; Indels 801; Gaps ::||: | : 2221 ASESASTSASASASTS 2236 2822 STESSGTOSPKRHSGS 2837 В ò 6 6 6 6 δ 9 & 9 9 <u>ک</u> م ð 엄 ઠે

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OY 2758 ERTPFSSSSSKHISSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVNNNT ::		Db 2475TSP8TSSSI8SGPDSP 2490	RESULT 14 E88320 Protein F07All 6 [imported] - Caenorhabditis elegans	Species: Caenorinaballis elegans Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001 Accession: E88302 and Sequencing Consorrium	form for	w_sanger. Science		Alcross-Tereferences: GB:CDF_11; F1DN:CAA93781.1; P1D:g3881547; GSPDB:GN00020 C:Genetics: A;Gene: F07A11.6 A:Man nosition: 2	ry Match  2.9%; Score 426.5; DB 2; Length 2738;  2.0cal Similarity 18.5%; Pred. No. 1.4e-09;	SDNFNTGNMTVLSPYLNTTVLPSSSSRGSLDSSRSEXDRSLERERGIGL	871 GTSSKRGLQISTTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHC	928 AHTHSNITYNFTKSENSNRTCSMPYAKLEYKRSSNDSLNSVSSNDGYGKRGQMKPS 1:	988 EDDESKFCSVQQYPADLAHKIHSANH	1043 PSQNERWARPKHIIEDEIKQS-EQRQSRNQSTTYPVYTESTDDKHLKFQP 535 QSPGYZFLESKEIKOBFSPTTSSASSSDLEIMEMPNPITRWIFFRWIRFRWING	6 QECVSPYRSRGANG    : 9VSSF	1140 PTNYSERYSEEGH	1200 SSSGQSSKTEHMSSSSEN	682 FAGG 1254 INQE	717HSLCIGPMTPSTPFPTSQPLLVWTTHLPGTSQ

A/Map position: 16	2374 QY 1255 1974 Db 50 2428 QY 1315 2034 Db 95 2461 QY 1375 2094 Db 139 2497 OA 1430	2549 Db 198 2207 Db 258 2606 Qy 1513 2267 Db 318 2666 Qy 1550 2315 Db 318 2720 Qy 1610 2357 Db 378	2753 QY 1668 2427 Db 470 2797 QY 1726 2480 Db 511 QY 1784 Db 560	Oy 1842 SPHHYTPIEGTPP   Oy 1842 SPHHYTPIEGTPP   Oy 1842 SPHHYTPIEGTPP   Oy 1902 SNOCSANTOALI   Oy 1902 SNOCSANTOALI   Oy 1902 SNOCSANTOALI   Oy 1903 SNOCSANTOALI   Oy 1959 TPVCFSHNSSLSS   Oy 1959 TPVCFSHNSSLPPPI   Oy 1959 SSSPETRSRTPPPI   Oy 1959 SSSPETRSRTPPI   Oy 1959 SSSPETRSRTPPPI   OY 1959 SSSPET
2173	2315 QPLSRPIQSPGENSISPGENGISPPNKLSQLPRTSSPSTASTKSSGSGKWSYTSPGRQMS	2095 BOFPGL'SSYINRDSIGATNGVLHLPTOSIQR'PSS'-TASTSSN'PRAPLQPSAS'VNOWTID 2498SVQGGWRKLPPNLSPTIEYNDGRPARHDIARSHSESPSRLPINRSGTWKR 2154 PABIEETRVQRWFYKPLKA'SABBAATVMAVASSDPNPPATSTVDLAAMLQQLQA 2550 -EHSKHSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQV 250 -EHSKHSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQV 250 - AKGTWRKIKENEFSPTRSTPOPLSNLETLSTASLANLATGGALNPLSKLADTSSLNQSSP 2607 SAKGTWRKIKENEFSPTRSTSQTVSSGATNGAESKTLIVQMAPAVSKTEDVWRIEDCPI 2268 VYQGIARVLLTWNMGQMLATHQTSELLATMN-QQETLMALLAARNGLPF 2667 NNPRSGRSPTGNTPPPVIDSVSKRANPNIKDSKDNGAKQNVGNGSVPMRTVGLEN 2667 NNPRSGRSP	2721 RITSFIQVDAPDQXGTEIKPGQNNPVPVSETNE	RESULT 15 T02345 T02345 T02345 T02345 T02345 T0345 T0346 T0346 T0362 T036216181 T0362 T036216181 T0363 T0362 T036216181 T0363
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tive 259; Mismatches 742;
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OM protein - protein search, using sw model

August 25, 2004, 16:58:21; Search time 32.5 Seconds (without alignments) 4554.937 Million cell updates/sec Run on:

US-09-442-489F-2 14575 1 MAASYDQLLKQVEALKMEN......ESSGTQSPKRHSGSYLVTSV 2843 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Nakamura Y., Horii A.;
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mutations in very well differentiated adenocarcinoma and signet-ring
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results in a severe desmoid phenotype and is associated with
overexpression of beta-catenin in the desmoid tumor.";
Clin. Genet. 57:205-212(2000).
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Marbitne 201384842; PubMed=10926498;

Day C.L., Alber T.; d. the mino-terminal coiled-coil domain of the
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"Molecular mechanisms of beta-catenin recognition by adenomatous
polyposis coli revealed by the structure of an APC-beta-catenin
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Nagase H., Miyoshi Y., Horii A., Aoki T., Petersen G.M.,
Vogelstein B., Maher E., Ogawa M., Maruyama M., Utsunomiya J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APC tumor suppressor.";
J. Mol. Biol. 301:147-156(2000).
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"Hum. Nater. 1147-7171992).

"Tistyr may repeate the first is a south with the control of 150 unrelated patients.",

"Mobile Pripheral Blood lymphocytes;

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                                                                           Kakiuchi H., Watanabe M., Vabijima T., Toyota M., Imai K.,
Weisburger J.H., Sugimura T., Nagao M.;
Weisburger J.H., Sugimura T., Nagao M.;
Specific S-/GGA-3.
Segana T., Sugimura T., Nagao M.;
Specific S-/GGA-3.
Segana T., Sugimura T., Nagao M.;
Proc. Natl. Acad. Sci. U.S.A. 92:910-914(1995).
-! PUNCHION: Tumor suppressor. Promotes rapid degradation of CTNNB1
and participates in Mrt signaling. APC activity is correlated with its phosphorylation state (By similarity).
-! SUBUNIT: Forms homooligomers. Associates with catenins. Binds axin (By similarity).
-! PTM: Phosphorylated by GSK1B (By similarity).
-! PTM: Phosphorylated by GSK1B (By similarity).
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Wnt signaling pathway: Anti-oncogene; Phosphorylation; Coiled coil;
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62 COLLED COLL (POTENTIAL).
260 COLLED COLL (POTENTIAL).
493 ARM 1.
589 ARM 3.
636 ARM 4.
681 ARM 5.
723 ARM 6.
723 ARM 7.
1155 ARP/GLU-RICH (ACIDIC).
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11891 HIGHLY CHARGED.
523 C->R: IN AN IQ-INDUCED COLON TUMOR.
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                                            and Fischer 344/N;
[2]
STRAIN-Sprague-Dawley, and Fischer
MEDLINE-95148647; PubMed=7646077;
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InterPro; IPR008938; ARM.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 4.
SWART; SM00185; ARM; 5.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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STRAIN=Fischer 344/N; TISSUE=Brain;
MEDLINE=96116966; PubMed=8553176;
MONITINE=96116966; PubMed=8553176;
TOYOTA M., UShijima T., Kakiuchi H., Watanabe M., Imai K., Yachi A., Sugimura T., Nagao M.;
"CDNA cloning of the rat APC gene and assignment to chromosome 18.";
Mamm. Genome 6:746-748(1995).
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Adenomatous polyposis coli protein (APC protein).
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NFDWKAIQEGANSIVSSLHO-AAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEE LQANMPSISRGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGQTATTSFRGAKP ASKGINOMINGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQSTFIKEAPSPTLRRKL GFSCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTID GFSCSSLSALSLDEPFIQNDVELRIMPPVQENDNGNETEPEQPEESNENQDKEVER-D 1677 VQSGEFEKRDTIPTEGRSTDEAQRGKVSSIAIPDLDGSKAEEGDILAECINSALPKGRSH NRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFALENTPVCFSHNSSLSSDIDQE SVKSELSPVARQTSQLGGSSKAPSRSGSRDSTPSRPAQQPLSRPLQSPGRNSISPGRNGI PPPPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPD **AQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSH** 

Thu Aug 26 06:02:22 2004

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ARM 5.

ARM 6.

ARM 7.

SER-RICH.

ASP/GLU-RICH (ACIDIC).

ASP/GLU-RICH (ACIDIC).

HIGHLY CHARGED.

Missing (in isoform 2 and isoform 4).

/FIId=VSP_004116.
                                                                                                                                                                                                                                                      Isoid=Q61315-4; Sequence=VSP 004116, VSP 004117;
-!- TISSUE SPECIFICITY: Expressed in liver, spleen, kidney, heart, lung, brain, stomach, intestine, testis and ovary.
-!- PTM: Phosphorylated by GSK3B (By similarity).
-!- PTM: Contains 7 ARM repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (in isoform 3 and isoform 4).
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R PIR; 149505; 149505.

R HSSP; 002248; 149505.

R GO; 002057; ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCOUNTY, ACCO
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R INTERPO; IPRO00238; ARM
R INTERPO; IPRO00225; Armadillo.
R Pfam; PF00514; Armadillo.seg; 4.
DR PROSTIE; PS50176; ARW REPEAT; 1.
DR PROSTIE; PATCHWAY, ARM; SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, SAME, 
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                                                                                                                                                                                                   IsoId=261315-3; Sequence=VSP_004117;
                                                                                                                                Name=2;
IsoId=Q61315-2; Sequence=VSP_004116;
                                                                                                     IsoId=Q61315-1; Sequence=Displayed;
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                             2457 EESASFESLSPSSRPDSPTRSQAQTPVLSPSLPDMSLSTHPSVQAGGWRKLPPNLSPTIE 2516
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MEDLINE=94061824; PubMed=8242607;
MEDLINE=94061824; PubMed=8242607;
MEDLINE=94061824; PubMed=8242607;
MAPC gene messenger RNA: novel isoforms that lack exon 7.";
Cancer Res. 53:5589-5591(1993).
-: FUNCTION: Tumor suppressor. Promotes rapid degradation of CTNNB1 and participates in Wnt signaling. APC activity is correlated with its phosphorylation state (By similarity).
-: SUBUNIT: Forms homooligomers. Associates with catenins. Binds
                                                                                                                                   2517 YNDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSA
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STAIN-CSTBL/6J, and CAST/EI; TISSUE-Brain;
MEDLINE-9226101; PubMed=1350108;
Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R.,
Luongo C., Gould K.A., Dove W.F.;
Multiple interinal neoplasia caused by a mutation in the murine
homolog of the APC gene.
Science 256:668-670(1992).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Dicker F., Lambertz S., Reitmair A., Ballhausen W.G.;
"The murine APC gene: alternative splicing of 5' untranslated
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Q61315; Q62044;
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Adenomatous polyposis coli protein (APC protein) (mAPC).
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Length 2845; 145CA73CF570A499 CRC64;

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Best Local Simil Matches 2566; C	Similarity 90.0%; Pred. No. 0; 6; Conservative 113; Mismatches 159; Indels 12; Gaps 10;	<b>q</b> 3	3GR
	MAAASYDQLLKQVBALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM 60 	3 8 8	
61	ASSGQIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSRBGSVSSRSGECSPVFMGSFPR 120 		TNYSERYSEEECHEEEEERPINYSIKYNEEKHYDQPIDYSEKYATDISSGKESFSK 119
121	RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLONLTKRIDSLPL 	yo da	SENTSTP
181	OTDLITROLEYEAROIRVAMEBOLGTCODMEKBAORRIARIOOIEKDILRIROLLOSQAT	çç qa	1260 QTYCVBDTPICFSRCSSLSSAEDBIGCNQTTQBADSANTLQIABIKGKIGTRSAEDP 1319
241	EAERSSONKHETGSHDAERQNEGOZVGEINWATSGNGOGSTTRMPHETASVLSSSSTHSA 30	λ <sub>o</sub> q	VSEVPAVSQHPRIKSSRLQGSSLSSESARH-KAVEFPSGAKSPSKGGAQTPKSPPEHYVQ :
301	PRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL 36	oy.	1379 ETPLMFSRCTSVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKT 1438
3 61 6	HONDKDSVLGNRSKEARARASALHNIIHSOPDDKRGRREIRVLHLEGIRAYCETC 42 HONDKDSVLGNSKEARARASAALHNIIHSOPDDKRGRREIRVLHLEGIRAYCETC 42 HONDKDSVLGNSKEARARASAALHNIIHSOPDDKRGRREIRVLHLEGIRAYCETC 42 HONNYGGNI GASPGGGGGGBBSARA NAIHONA HONDKAGBBFIGNI HIIHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Vy qq	1439 PPPPPQTAQTKREVPXXXAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPD 1498 
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541	OCUTASVILANDEN SAVIDANI SAVIDA	δλ Qū	1619 PSQNELQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGG 1678
601	GY INSTRUCTOR VARIATIEN VER VALUE CALLE VALUE INC. 1997	ζ Q Q	1679 AQSGEPEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSH 1738
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721	GSAAALRIUMANRPAKKKOANKUISENESELEKURKOKALEARIUMAKEETEININISKUITEEN TE 	QJ QD	1799 LNAERVFSDNKDSKKONLKONSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSR 1858
781	SOMERINATE MANTE PARTICULAR TRANSPORTED FOR THE STATE OF	ζζ QΩ	1859 NDSLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQOSANKTQAIAKQPI 1918 
841	LDSSRSEXDRYCHRYQUIGGIAF DANNADDONGSDRYFIGNITYDGF DAN I VEGSGSSAGG 903	QY QD	1919 NRGQPKPILOKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSDIDQE 1978
901	DUSSESENTELHCYDERNALRRSSAAHTTENAGISSERGEQITTTAAQIAKVMEEVEALHIS 89 OEDRSSGSTTELHCYTDERNALRRSSAAHTTHSNITVNFTKSENSNRTCSMPYAKLEYKRSS 96 DIR THE THE TEST OF THE TEST O	ço da	1979 -NNNKENEPIKETEPPDSGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDD 2037
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                                                                                          LQANMPSISRGRIMIHIPGVRNSSSTSPVSKKGPPLKTPASKSPSEGQTATTSPRGAKP
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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J. Biol. Chem. 267:16561-16566(1992).
-!- FUNCTION: Structural protein involved in the filamentous cross-
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MEDLINE=92355629; PubMed=1379599;
Langkopf A., Hammarback J.A., Mueller R., Vallee R.B., Garner C.C.
"Microtubule-associated proteins 1A and LC2. Two proteins encoded
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MAPA_RAT

ID MAPA_RAT

C P34926;

D7 01-FEB-1994 (Rel. 28, Created)

D7 01-FEB-1994 (Rel. 28, Last sequence update)

D7 16-CCT-2001 (Rel. 40, Last annotation update)

E Microtubule-associated protein 1A (MAP 1A) [Contains: MAP1 light on the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the contains of the con
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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bridging between microtubules and other skeletal elements.
-!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate with MAPIA and MAPIB proteins.
-! TISSUE SPECIFICITY: BRAIN, HEART AND MUSCLE.
-!- DEVELOPMENTAL STRAGE: EXPRESSED LATE DURING NEURONAL DEVELOPMENT APPEARING WHEN AXONS AND DENDRITES BEGIN TO SOLIDIFY AND STABILIZE
                                                                                                                                                                                                                                                                                                                                               DOMAIN: THe basic region containing the repeats may be responsible for the binding of MAPIA to microtubules.

From: Various serine residues may be phosphorylated by cAMP kinase. PTM: LC2 IS COEXPRESSED WITH MAPIA. IT IS A POLYPEPTIDE GENERATED FROM MAPIA BY PROTECLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH BOTH MAPIA AND MAPIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----RNVSSLIATN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAPI LIGHT CHAIN LC2.
LYS-RICH (BASIC).
11 X 3 AA REPEATS OF K-K-[DE].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299526 MW; 3DEF74427BA9D7D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.3%; Score 477; DB 1; Le
ilarity 18.7%; Pred. No. 2.4e-10;
Conservative 359; Mismatches 1039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       609 VDGALAFLVGTLTYRSQT----NTLAIIE--SGGGIL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M83196; AAB48069.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: TO MAPIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A43359; A43359.
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440
444
449
539
2774 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microtubule; Repeat;
CHAIN ?2465 27
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Best Local Similarity
Matches 542; Conserv
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420
424
424
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1713 LDDNKAEEGDILAECINSAMP	1378 QKGRDLDEKDTAAELDKGPEP	1773 ISPVKPIPQNTEYRTRVRKNAI		RVRGSFAFDSPHHYTPI		SEAKVISHI 		1947 - IDENLÇMFALENIFVCFSHW 		2000SKPQASGYAPKSFHVE					A		1759 FEIISPPASPPEMTGQRVPS-	2187	1817 PLPPAPLSPAPAPPTPAPEPH1	2223 SISRGRIMIHIPGVRNSSSSTS	1877 KAEGEREGEGGAGAPDŚŚFSI	2264GQTATTSPRG/	1937 YEQMMLTGLGPACPTREPPLGA	2309 PSRPACQPLSRPICS	1997 PAFSYASLAGPAVPPROEPI	2349 SSPSTASTKSSGSKMSYTSPC	2055 PDRRİPSPKETGRGHW	2406 NGNGANKKVELSRMSSTKSSGE	2104 HSSLWPETEAYSSLSSDSHLGS	2428ESDRSERPVLVRQST	2164 AFSGÖRALALVPGTÖTRTRHDE	2475TRSQAQTPVLSPSL	2224 LSEGSSSEATTPVISSVAERFI	2518 NDGRPAKRHDIARSHSESPSRI  :  : : : :	2279PSASLDLAPAPAPAPA	2567 TGSSSSILSASSESSEKAKSEI
λο -	đ	ò	q <sub>Q</sub>	ð :	<u>a</u> (	Š	9 8	<u></u>	3 8	à á	8 8	Š 1	g (	Š 1	g (	ð	<u>유</u>	à	đ	λ̈	đ	δλ	<u>유</u>	č	q <sub>O</sub>	λo	đ	ò	đ	λõ	QC Op	δ	qq	ò	da .	λΌ.
932 SNITVNFFKGRNGNRTCMDVAKI, EVKB.SGNDGI MSUSGNDGV 973	RRLIKDKAGKKHLKEKISKLEEKKDKEKKEIKKEEKKELKKEEGRKEEKK		442 DAK	1029 LKYSDEQLNSGRQSPSQNERWARPKHIIEDFIKQSEQRQSRNQST 1073	:     :     :     :     :     :     :     :       :	1074 TYPUYTESTDDKHLKFQPHFGQQECVSPYRSRGANGSETNR 1114	552 TGLGEKPLPADATEQGHPSAAIQVTQPSGPVLEGEHVEREKEVVP-DSPGDKGS-TNRGP 609	1115VGSNHGINQNVSQSLCQEDDYEDDKPTNYSERYSEED 1152	610 DSGAEVEKEKETWEERKQREAELGPENTAAREESEAEVKEDVIEKAELEEWEETHPSDEE 669	1153 HEEEERPINYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSKSKGSG 1203	670 GEETKAESFYQKHTQEALKASPKSREALGGRDLGFQGKAPEKETASFLSSLAT 722	1204 QSSKTEHMSSSSENTSTPSSNAKRQNQLHPSSAQSRGQPQ 1244	723 PAGATEHVSYIQDETIPGYSETEQTISDEEIHDEPDERPAPPRFPTYYDLSGPEGPGPF 782	1245 KAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSAEDRIGCNQTTQEADSANTLQI 1304	:     :     : :     : :       : : :       : : : :       : : :       : : :       : : :       : : :       : : :       : :       : :       : :       : :       : :       : :       : :         : :	1305 AEIKGKIGTRSAED-PVSEVPAVSQHPRTKSSRLQGSSLSSBSARHKAVEFPS-GA 1358	TSVAEDQSVASLTAPQTEETGKSSLLLDTVTSIPSSRTEATQGLDYVPSAGT	1359 KSPSKSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFESRSIASS 1404	:   :   :               : : ISPISSIEEDKGFKSPPCEDFSVTGESEKKGETVGRGESGEKAVGKE	VQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPP	: :    BPALGEVEERCLSPDDSTVKMASPPP	PPQTAQTKREVPKNKAPTAEKRESGPKQA	994 SGPPSAAHTPFHQSPVEDKSEPRDFQEDSWGETKHSPGVSKEDSEEQTVKPGPEGG 1049	1471AVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSSLSA 1508	1050 TSEEGKGPPTRSPQAQDMPVSIAGGQTGCTIQLLPEQDKAIVFETGEAGSNLGA	1509 LSLDEPFIQKDVELRIMPPVOENDNGNETESEOP 1542	:   :   :   :   :   :		1162 CSLKEQOSHKDLWPWVSPEDTOSLSFSEESPSKETSLDISS	1600 KLPPPVARKPSQLPVYKLLPSQNRLQPQXHVSFTPGDD		1638 MPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGE	:   :     ::     ::     1.1   1.2   1.3	1674 GVRGGAQSGEFEXRDTIPTEGRSTDEAQGGKTSSVTIPE 1712	:   :   :	
ò	7 A	ò	q <sub>Q</sub>	ζ	qq	ò	qa	δõ	q	δλ	qq	λö	q	δ	QD ,	ò	qa	ò	- <b>ਪ</b> ਹ	δ	අු	ò	qa	ð	. d	ò	· 연	δ	ପୁ	ò	đ	δ	: A	ò	đ	

1713	LDDNKABEGDILABCINSAMPKGKSHKDFRVKKIMDOVQQASASSSAPNKNQLDGKKKKP 1772	0 0
1773	TSPVKPIPQNTEYRTRVRKNADSKNNLNABRVFSDNKDSKKQNLKNNSKDFNDKLPNNED 1832	0 0
1833	CFSRNDSLSSLDFDDDDVDLSREKAELRKAKENKE 188	o ⊢
1890	SEAKVTSHTELTSNQOSANKTQAIAKQPINRGQFKPILQKQSTFPQSSKDIFDRGAA 1946	9 9
1947	-IDEKLQNFAIENTPVCFSHNSSLSSLSDIDQENNN-KENEPIKETEPPDSQGEP 1999 	ē 0
2000	SKPQASGYAPKSFHVEDTPVCFSRNSSLSIDSEDDLLQECI-SSAMPKK 205G QKEPVPAWEGKSPEQEVRYWRDRDITLQQDAYWRELSCDRKVWPPHELDGGGARPRYCE 1690	0 0
2051	KKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSFDSENFDWK 2102	ū o
2103	AIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKP 215E	ထ ထ
2159	FTSNKGPRILKPGEKSTLETKKIESESK	ω ω
2187	PLPPAPLSPAPAPTPAPEPHTPVPFSWGLESVVAAVQEGAAELEGGPYSPLGKDYR 1876	64 65
2223	SISRGRIMIHIPGVRNSSSTSPVSKKGPPLKTPASKSPSE 2263 	m w
2264	GQTATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDST 2306 YEQMMLTGLGPACPTREPPLGASGDWPPHLSTKEEAAGCNTSAEKETSSPASPQNLQSDT 1996	ളയ
2309	PSRPAQQPLSRPIQSPGRNSISPGRNGISPPNKLSQLPRT 234E	∞ 4 <sub>1</sub>
2349	240	ന ന
2406	NGNGANKKVELSRMSSTKSSGS 2427 : : :           HSSLMPETEAVSLSGISGISHLGSVRPSLDFPASAFGFSSLOPAPPOLPSPAEPRSAPCGSL 2162	r 6
2428	247	44 W
2475	TRSQAQTPVL.SPSLPDMSLSTHSSVQAGGWRKL.PPNLSPTIEY 2517	r
2518	NDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRR 256	90 90
2567	TGSSSSILSASSESSEKAKSEDEXHVNSISGTKQSKENQVSAKGTWRKIKENEF 2620	0

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[8]
FUNCTION
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    2436
                                                                                                                                                                                                                                                                                                                                      2799
TKKPSPFLSPSGD--HEANGPGETSLNPPGFVTATAEKEEAEAPHAWERGSWPEGAERSS 2376
                                                                                                                                                       2709
                                                                                                                                                                                                                                               2710 SVPMRTVGLENRLTS----FIQVD-APDQKGT-BIKPGQN-NPVPVSETNESP---IV 2757
                                                                                                                                                                                                                                                                                                                                                                   2554 MADPEGLSSESGRVERLREKGRPGRRAPGRAKPASPARRLDIRGKRSPTPGKGPVDRTSR 2613
                                                                                            2655 EDVWVRIEDCPI---NNPRSGR-SPTGNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNG
                                                                                                                                                                                                  2437 DDSDLSTEEARLAGKGGRRRVGRPGATGGPCPMAD---ETPPTSASDSGSSOSDSDVPPE
                                                                                                                                                                                                                                                                           2758 ERTPFSSSSSS-----KHSSPSGTVAARVTPFN------YNPSPRKSSADSTS-
                                                                  -------APAVSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 3 AND 4), FUNCTION, ALTERNATIVE PROMOTER USAGE, TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, AND MUTANTS B9 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Embryo;
MEDLINE=20157049; PubMed=10655223;
Rebay I., Chen F., Hsiao F., Kolodziej P.A., Kuang B.H., Laverty T.,
Sub C., Voas M., Williams A., Rubin G.M.;
"A genetic screen for novel components of the Ras/mitogen-activated
protein kinase signaling pathway that interact with the yan gene of
Drosophila identifies split ends, a new RNA recognition motif-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLIN3=20025936; PubMed=10556062;
Wiellette E.L., Harding K.W., Mace K.A., Ronshaugen M.R., Wang F.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "spen encodes an RNP motif protein that interacts with Hox pathways to repress the development of head-like sclerites in the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20171275; PubMed=10704397; Kuang B.H., Wu S.C.-Y., Shin Y.-A., Luo L., Kolodziej P.A.; Suang B.H., Wu S.C.-Y., Shin Y.-A., Luo L., Kolodziej P.A.; Split ends encodes large nuclear proteins that regulate neuronal cell fate and axon extension in the Drosophila embryo."; Development 127:1517-1529(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1), SUBCELLULAR LOCATION, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopteraygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                  2621 SPTN--STSQTVSSGAINGAESKTLIYOM-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPEN DROME STANDARD; PRT; 5560 AA. 088X83; 09NHA1; 09NJ7; 09U6C3; 09VPL1; 09VPL2; 110-0CT-2003 (Rel. 42, last sequence update) 110-0CT-2003 (Rel. 42, last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2614 TVPRPRSTPSQVTSAEEK 2631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jevelopment 126:5373-5385(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                              --ARPSQIPTPVNNNTKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contaîning protein.";
Genetics 154:695-712(2000).
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SPEN OR CG18497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WCBI_TaxID=7227;
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                       2319
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Admans N.D., Centiker S. E. Holt R.D. Standel N.D., Hobskins R. A., Galler B.P.,
Admans I.G., Scherer S.E., Nichards S., Ashburnor M., Henderson S.N.,
Statcon G.G., Worthan J.R., Andels N.D., Zhang O., Chen L.D.,
Statcon G.G., Worthan J.R., Andels N.D., Zhang O., Chen L.D.,
Standon R.D., Chen L.D.,
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Standon R.D., Standels N.D., Standels N.D., Chen L.D.,
Standon R.W., Bench B.W., Banck E.G., Half J.G., Nation C.R., Nathor G.L.G.,
MR. K.H., Doylo, C., Saxer E.G., Half J.G., Nation C.R., Nathor G.L.G.,
Bandon R.Y., Bench B.W., Bouck J. Brocketein P., Brother P., Chandra I.,
Bardon R.Y., Bench B.W., Bouck J., Brocketein P., Brother P., Chandra I.,
Barton R.Y., Bould J.E., Downes M., Dowles D., Brocketein P., Brother P., Chandra I.,
Gerry J.M., Cawley S., Dahles C., Daverport L.B., Davies P.,
Borkova D. Bocchan M.R., Bouck J., Brocketein P., Brother P., Chandra I.,
Gerry J.M., Cawley S., Dahles C., Charles E., Charles E., Chandra I.,
Gerry J.M., Cawley S., Dahles C., Charles E., Calles E., Charles E.,
Borkova D. Houston K.M., Houland T.J., Wei M.H., IDegan C.,
Andlai M., Kalles E., Goorrell J.H., Ou Z., Gaant P., M.H., IDegan C.,
Andlai M., Kalles E., Charles T., Berland T.J., Wei M.H., IDegan C.,
Andlai M., Kalles E., McChen T., Sandore R.D., Merkel D. J., Morth T.,
Andlai M., Kalles E., McChen T., Sandore R.D., Neither D. J., Morth T.,
Andlai M., Kalles E., Kadhra C., McCheller E., Mennel D.L.,
Malson B., Weiner S., N., Woodag T., Wolley K.C., Mollard J., Mangh A.H., Mang A.,
Milliams S.M., Woodag T., Wolley K.C., Mu D., Yang S., Yang S., Man K.H.,
Respitation of the Drosophila melanogaster W., Reliams D., Mang S.,
Milliams S.M., Woodag T., Wolley K.C., Mu D., Yang S., Man K.H.,
Respitation of the Drosophila melanogaster W., Reliams D., Mang S.,
Milliams S.M., Woodag T., Wolley K.C., Mu D., Yang S., Nan K.,
Milliams S.M., Woodag T., Wolley B., Marph M., Phulley B., Marph M., Phulley B., Marph M., Man
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                                                                                                                                                    Query Match
Best Local Similarity 18.2%; Pred. No. 6.5e-10;
Matches 640; Conservative 498; Mismatches 1307; Indels 1065;
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PROSITE; PS50917; SPOC; 1.
Transcription regulation; Repressor; Developmental Nuclear protein; Repeat; RNA-binding; Coiled coil; Alternative promoter usage; Alternative splicing. DOWAIN 554 632 RNA-BINDING (RRM) 1. DOWAIN 656 730 RNA-BINDING (RRM) 2. DOWAIN 734 806 RNA-BINDING (RRM) 2.
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3497 TVPAGLPPSPVKIEPPT1 1662 IBSPPNELAAGBGVRGGF 3553 ISCNISAASATASASF 1708 - VTIPELDDNKAEBGDII ::       :     :     3612 TISIPECTPHFAVPQWVI 1765 LDGKKKKPTSBV   3663 AQSRLVGQLSPVGRPMVG	1811 SKKONLKUNSKDFNDKLE  3722 SPTTSKVNSYOPRNOQVE  1848PIEGTPYCFSRNDSLE  3782 VQPQQATQSQVASSPPLC  1896  3833 MQQFWHQQMIQRQQHWQC  1914 AKQPI  3893 QQPPTQKQHQAQQFNQC  1946 ATDEXLQNFSC  1955 AQQQLQQIQQLQQLRGHGB  1956 AQQQLQQIQQLQQLRGHGB  1956 AQQQLQQIQQLQQLRGHGB  2040 KKKRPSRLKGDNEKASP  2105 GGGANSIVSSLHQAAAA  2105 QGGANSIVSSLHQAAAA  2105 QGGANSIVSSLHQAAAA  2105 QGGANSIVSSLHQAAAA  2105 QGGANSIVSSLHQAAAA  2105 QGGANSIVSSLHQAAAA  2105 QGGANSIVSSLHQAAAA  2156 EKPFTSNKGPRILKFGBR  2156 EKPFTSNKGPRILKFGBR  2156 EKPFTSNKGPRILKFGBR  2156 GRAPGAGGSAKGGQPR  2258 SKSPSEGGATTSPR  2258 SKSPSEGGATTSPR  2316 PLSRPIQSPGRNSISPGR  2316 PLSRPIQSPGRNSISPGR  2316 PLSRPIQSPGRNSISPGR  2316 PLSRPIQSPGRNSISPGR  2316 PLSRPIQSPGRNSISPGR  2316 PLSRPIQSPGRNSISPGR  2317 PTSSVLTAAEKKARNOJ  2420 SSTKSSGSESBRSERPVI	2480 QTPVLSPSLPDMS               4482 QSEVISNTDPIGGDNSES
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	266 ADTSAACTPLYMTPAITSELEDINGSSERCHAFORFORDICKHESSELFERSTEED 2140EKHERKEKKERNENTGATVENSPTINDTSSEKCHAFORFORDICKHESSELFERSTEED 2140EKHERKEKKERKLENNTEATVENSPTINDTSSEKGAKEEBHRIKKSKEKSKEND 2151 BESPECSYOPPADLAHILIB	343/ IDETVQSSSSFEKSISNNSFIFKEIANIDIFNVESQFKLSNESIFVESVIIKLFFFULFR 1617LLPSQNRLQPQKHVSFTPGDDMPRVYCVBGT-PINFSTATSLSDLT
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3497	TVPAGLPPSFVKIEPPTISKLQQPLVQPVQTVLPAPHSTGSGISANSVINLDLSNV 3552
1662	IESPPNELAAGEGVRGGAQSGEFEKRDTIFTEGRSTDEAQGGKTSS 1707
3553	GPITPQ-QAI
1708	-VTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSAPNKNQ 1764
3612	TISIPEQTPHFAVPQWLSPQSHHPQQPGTYWGIRAPSPHSPLHSPGRGV 3662
1765	LDGKKKKPTSPVKPIPQNTEYRTKVRKNADSKNNLNAERVFSDNKD 1810
3663	PSPQQQVQQTQQQHALITSPQSSNISPLASP
1811	SKKONLKNNSKDFNDKLPNNED1847
3722	SPITSKVNSYOPRNOQVPQOPSPKSVAEVQTIPQLMTIPLQKMTPIQVPHHPTIISKVVT 3781
1848	EKAELR
3782	VQPQQATQSQVASSPPLGSLP-PHKNVHLNAHQNQQPQVIAKMTAHQHQQH 3832
1898	
3833	MQQFMHQQMIQRQQHMQQQQLHGQSQQITSAPQHQMHQQHQQHQQQQQQQHHNQQHLHQQLHA 3892
1914	AKQPINRGQPKPILQKQSTFPQSSKDIPDRGA 1945
3893	GOHPTQKGHQAQQQFNQQ1QQHQSQQQHQVQQQQHQVQACHQSQQQLNQQHQ 3949
1946	ATDEKLONFAIENTPVCFSHNSSLSSLSDIDQENNNKENEPIKETEPPD- 1994
3950	AQQQQLQQLQXLQQMHGPQQQQXSPQGVGHLGGSTSIFASQQHNSQLPARGVPQQQHPQQ 4009
1995	KSFHVEDTPVCFSRNSSLS
4010	LSHSSPCKPNTLVSVNQGVQPPAIL
2049	
4060	
2105	QEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQE 215
4114	-QGKDSTPPGHVEPTPAMSAQKTSESVSVIRTPTTTGLAVISANTVGS
2156	Ħ
4162	LITERNLIKISOPKODELIEODSKEVDSDYWSAKEVNIDSVIKKLDTPLASKDAKRAV 4219
2212	QMKQPLQANMPSISRGRTMIHIPGVRNSSSSTSPVSKKGPPLKTPA 2257
4220	EMÇALAPAPIFNYÇYGNÇSMAÇETALFILOMSVNNSNDADIDDELETRÇEFFANFFILTV *2.7
2258	SKSPSEGQTATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPSKSGSKUSTFSKFAQQ 231
4280	GRPPGRGGSAKRGRQPRGAKKVGGFPLNSVIAAPPGVDSLVVQPGDNGVQI 433
2316	PLSRPIQSPGRNSISPGRNGISPPNKLSQLPRTSSPSTASTKSS   :  :
4331	RİRKPVTAPVTRĞRKÖRPPRNILİLÖQQQLQQQQLDIQRKGMEMVTSATSSTPLPTP 4386
2360	GSGKMSYTSPGRQMSQQNLTKQTGLSKNASSIPRSESASKGLNQMNNGNGANKKVELSRM 2419
4387	
2420	SSTKSEGSESDRSERPVLVRQSTFIXEAPSPTLRKKIBESASFESLSPSSRPASPTRSQA 2479
4437	
2480	QTPVLSBSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDGRPAKRHDIARSH
4482	

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OF 2002-3664 FROM N.A.

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                                                    LPKGAOTPPRRSG--RNAQAKKTDAVQIINAVGRPRRSKDRKTIGEOTANLIEEVTASNA 4595
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4823 QQ------QPQ-IVAPAKQPIILQQNPLPTVLHHAQHTVRPPQPLKAHVLNRE 4870
                                                                                                                                                                                                                                                                                                  : : : : : : : CUITAGMPQGKEGNLPAATAAAPANS--SNEDGQAAPPPQLGHQQQQQQHP--QQPPQQQ
                  ---TGSSS
                                                                                                                                         4596 TVAASHLAPPEGAGVESHVPQLDAKEVEPVSVVTPISTPAPVSVAAPVTVPVPAMVPVKP
                                                                                                                                                                                    ---KOSKENQVSAK--GTWRKIKENEFS---PTNSTSQTVSSGATNG---AESKTLIYQM
                                                                                                                                                                                                                                                                         2648 APAVS-----KTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDNQ
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9096T58; Q9H9A8; Q9NWH5; Q9UQ01; Q9Y556;

10-OCT-2003 (Rel. 42, Created)

10-OCT-2003 (Rel. 42, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

MSX2-interacting protein (SMART/HDAC1 associated repressor protein).

MINT OR SHARP OR KIAA0929.

Home sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, INDUCTION, RNA-BINDING, AND INTERACTION WITH NCOR2; HDAC1; HDAC2; RBBP4; MBD3; RAR AND MTAIL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEÇUENCE OF 793-1595 FROM N.A., AND VARIANT PRO-1091.

TISSUE-Embryo, and Teratocarcinoma;

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,

Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NOBI_TaxID=9606;
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MEDLINE=21231190; PubMed=11331609;
Shi Y., Downes M., Xie W., Kao H.-Y., Ordentlich P., Tsai C.-C.,
Hon M., Evans R.M.;
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repression and activation.";
Genes Dev. 15:1140-1151(2001).
                                                                                                  SILSASSESSEKAKSE ----- DEKHVNSISGT-------
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Rhodes S., Huckle E.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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                2533 SESPSRLPINRSGTWKREHSKHSSSL-
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	1138 DKPTNYSERYSEEBQHEEEBRPTNYSIKYNBEKRHVDQPIDYSLKYATDIPS-SQKQS 1194  100 REREREREREREPSDRDHERRPIERSQSPWILRRPQSPGASPSQAERLPSDSERRL 755  1195 FSFSKSSGQSSKTEHMSSSSENTSTPSSNAKRQNQLHPSSAQ 1237  126 YSLSSDRSGSSLSPPRYEKLDKSRLERYTWSETFDPERVERRERILIKERVE 815  1238SRSGQPOKAATCKVSSINQTIOTYCVEDTPICFSRCSSLSSLSSBEDBIGCNQTTQB 1295  816 KDKTDKQKRKGKVHSPSSQSSETDQENERBQSPEKPRSCOKLSRESADBIGCNQTTQB 1295  1296 ADSANTLQIABIKGKIGTRSAEDPPVSEVPRVSQNRLSSRLQGSSLSSESAR 1348  872 LELMPCVVLTRVKEKEGKVIDHTPVEKLKAKLDNDTVKSSALDQKLQVSQTEPPAKSDLSK 931	1349 HKAVEFBGGAKSPSKSGAQTPKSPPEHYVOETPLMFSRCTSVSSLDSFESR 1399  13. LESYRMKVPREKGLSSHVEVVEKEGRLKARRHLKPEQPADGVSAVDLEKLEARKRR 987  1400 SIASSVQSEPCSGMVSGIISPSDLPDSPGGTMPPSRSKTPPPPPPQTAQTKREVPKNK 1456  1988 FADSNLKAEK	PEREDVRKANY CSLRDETPERKSGOEKSHSVNYEEKIGIDIDHTQSYRKQMEQSRRK POKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPENELAAGEGV    COMEMBIAKSEKFGSFKKDVDEYERRSLWHEVGKPPQDVTDDSPPSKKRRMHUVDFD
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EMBL; AL034555; CAB85442.1; ALT_SEQ. EMBL; AL0456955; CAB85444.1; ALT_SEQ. EMBL; AL0456998; -; NOT_ANNOTATED_CDS. EMBL; AL096858; CAB31072.1; ALT_INIT. EMBL; AL096882; BAA91405.1; ALT_INIT. EMBL; AR000882; BAA91405.1; ALT_INIT. EMBL; AR002349; BAA91432.1; ALT_INIT. EMBL; AR023146; BAAA6773.1; - InterPro; IPR000504; RNA_rec_mot. PEBN; PF00076; rrm; 4. PROSITE; PS50102; RRM; 4. PROSITE; PS50102; RRM; 4. PROSITE; PS50102; RRM; 4. PROSITE; PS50103; RRM; RNP_I; FALSE_NEG.	Transcription regulation; Repressor; Nuclear protein; DNA-binding; Repeat; RNA-binding; Coiled coil; 3D-structure; Polymorphism.  DOMAIN 1 573 DNA-BINDING (RRM) 1.  DOMAIN 335 415 RNA-BINDING (RRM) 2.  DOMAIN 438 513 RNA-BINDING (RRM) 3.  DOMAIN 517 589 RNA-BINDING (RRM) 3.  DOMAIN 517 589 COILED COIL (POTENTIAL).  DOMAIN 1170 1191 COILED COIL (POTENTIAL).  DOMAIN 1408 1428 COILED COIL (POTENTIAL).  DOMAIN 1592 1612 COILED COIL (POTENTIAL).  DOMAIN 1928 1944 COILED COIL (POTENTIAL).  DOMAIN 1928 1944 COILED COIL (POTENTIAL).  DOMAIN 2221 2707 RID.	DOMAIN 2130 2464 INTERACTION WITH MSX2 (BY SIMILARITY).  DOMAIN 2130 2464 INTERACTION WITH REPSUH (BY SIMILARITY).  DOMAIN 125 277 ARG-RICH.  DOMAIN 2428 2570 FRCH.  DOMAIN 2428 2520 PRO-RICH.  DOMAIN 3220 3482 PRO-RICH.  VARIANT 1091 1091 L -> P (in dbSNP:848208).  // FIId=VAR_017120.  VARIANT 2360 2360 N -> D (in dbSNP:848210).  // FIId=VAR_017121.  CONFLICT 956 956 G -> D (IN REF. 4).  SEQUENCE 3664 AA; 402245 MW; 5228C58533E5B27B CRC64;	Section   1, 18   Secre 445;   DB 1;   Length 3664;     Set Local Similarity   19.2%;   Pred. No. 4.9e-09;     Liches 488;   Conservative   341;   Mismatches   970;   Indels 744;   Gaps   115;     226   REVRGREPERNYQHSRSRSPHSS

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MEDLINE=22579291; PubMed=12693553; SEQUENCE OF 2598-3644 FROM N.A. TISSUE RARARAR RELITER RARAR RELITER RELITER RELITER RAPARAR RELITER RARAR RELITER RE 2488 2261 2720 2321 VDKSASLKAVDAAVS---PRCAAAQAGERESGVVAVSPEKSESPQKEDGLSSQLKSDPVD 2143 2344 -PDMSLSTHSSVQA-----GGWRKLPPNLSPTIEYNDGRPA--KRHDIARSHSESPSRLP 2540 INRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSESSEKAKSED----EKHVNSIS 2596 2597 GTKQSKENQVSAKGTWRKIKENEFSPINSTSQTVSSGAINGAESKTLIYQ-----MAP- 2649 2187 2247 SHTELTSNOOSANKTO----AIAKOPINRGOPKPILOKOSTFPOS---SKDIPDRGAATD 1948 DHKEEBQERQELFASRFLHSSIFEQDSKRLQHLERKEEDSDFISGRIYGKQTSEGANSTT 1573 PKSFHVE-DIPVCFSRNSSLSSLSIDSEDDLLQECISSAMPKKKKPSRLKGDNEKHSPRN 2067 MGGILGEDLTLDLKDIQRPDSEHGLSPDSENFDWKAIQEGANSIVSSIHQAAAAACLSRQ 2127 ----PDSTQPLS 1760 2291 2345 LPRTSSPSTASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKNASSIPRSESASKGLNQM 2404 -----AVSKTE-----DVWVRIEDCPINNPRSGRSPIGNTPPV----------IDSVSEKANPNIK------DSKDNQAKQNVGNGSVPMRTVGLEN GMETDEAVSGILETEAATESSRPPVNAPDPSAGPTDTKEARGNSSETSHSVPEAKGSKEV 2721 RLTSFIQVDAPDQXGTEIKPGQNN-----PVP--VSETN----ESPIVE-----RT PFSSSSSSK-HSSPSGTVAARVT--PFNYNPS-----PRKSSADSTSARPSQIPTP | : | | | | : | | | | EPAETLKPPEGWRSPRSQKTAAAGGGPQGKKGKNEPKVDATRPEATTEV-GPQIGVKESSM 1761 K-----PAQKSEBANE-----PKAEKPDATADARPDANQKABAAPESQPPASEDLEVD 2405 NNGNGANKKVELSRMSSTKSSGSESDRSERPVLVROSTFIKEAPSPTLRRKLEESAS---ASSDSDSILSLKSGISLGSPFHLTPDQEEKPFTSNKGPRILKPGEKSTLETKKIESESKG 2188 IKGGKKVYKSLITGKVRSNSEISGQMKQPLQANMPSISRGRTMIHIPGVRNSSSSTSPVS KKGPPLKTPASKSPSEGQTATTSPRGAKPSVKSELSPVARQTSQ---------IGGSSKAPSRSGSRDSTPSRPA-----QOPLSRPIQSPGRNSISPGRNGISPPNKLSQ ----TRSOAQTPVLSPSL-----**EKLONFAIENTPVCFSHNSSLSSLSDIDQENNNKENEPIKETEPPDSQGEPSKPQASGYA** --FESLSPSSRPASP------2322 2248 1 1970 2029 2541 2087 2650 2683 2761 2462 2489 2009 2128 1949 1624 1667 1706 1753 2292

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Newberry B.P., Latifi T., Towler D.A., "The RRM domain of MINT, a novel msx2 binding protein, recognizes and regulates the rat osteocalcin promoter."; Biochemistry 38:10678-10690(1999). FUNCTION, SUBCELLULAR AND INTERACTION WITH MSX2 MINT MOUSE STANDARD; PRT; 3644 AA.

062504; Q80TN9; Q99PS4; Q90ZW2;
10-0CT-2003 (Rel. 42, Last sequence update)
115-MAR-2004 (Rel. 43, Last sequence update)
MSAZ-1nteracting protein (SMART/HDAC1 associated repressor protein)
MINT OR SHARP OR KIAA0929.
MNS musculus (Mouse) Craniata, Vertebrata, Euteleostomi; Sciurognathi, Muridae, Murinae, Mus. [1] -SEQUENCE OF 49-3644 FROM N.A. (ISOFORM 1), LOCATION, TISSUE SPECIFICITY, DNA-BINDING, VNNNTKKRDSKTDSTESSGTOSP 2831 VDEEPQARFRVHSIIĖSDPVTPP 2462 TISSUE=Testis; MEDLINE=99379811; PubMed=10451362; Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
NCBI\_TaxID=10090; 2440 2809 8 g

AGACHICE OF 1-112 FROM N.A.

Adachi J., Aizawa K., Akimura T., Arakawa T., Carninci P., Fukuda S., Adachi J., Aizawa K., Akimura T., Hori F., Imotani K., Hashizume W., Hayashida K., Hirozane T., Hori F., Imotani K., Konno H., Ishii Y., Itoh M., Kagawa I., Kawai J., Kojima Y., Kondo S., Konno H., Koya S., Miyazaki A., Murata M., Nakamura M., Nomura K., Numazaki R., Ohno M., Ohsato N., Saito R., Sakazume N., Sano H., Sasaki D., Sato K., Shibata K., Shiraki T., Tagami M., Takeda Y., Waki K., Watahiki A., Muramatsu M., Hayashizaki Y.; Subanitted (OCT-2002) to the EMBL/GenBank/DDBJ databases. Sakamoto T., Gotou T., Isagawa Y., Mimura H., Kimura K., Kawaichi "MINT/spen negatively regulates Notch signaling by inhibiting RBP-J/Su(H) activity."; Submitted (FBB-2001) to the EMBL/GenBank/DDBJ databases. SEQUENCE OF 69-3644 FROM N.A. (ISOFORM 2), AND VARIANTS THR-348; PHE-762; PHE-773 AND LEU-933. STRAIN=ICR; TISSUE=Brain; SEQUENCE OF 318-578 FROM N.A. rissum=Cochlea;

MEDLINE-3737053; PubMed-9119401;
Crozet F., El-Amraoui A., Blanchard S., Lenoir M., Ripoll C., Vac Hamel C., Fizames C., Levi-Acobas F., Depetris D., Mattei M.-G., Weil D., Pujol R., Petit C.;
"Cloning of the genes encoding two murine and human cochlear unconventional type I myosins.";

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Prediction of the coding sequences of mouse homologues of KIAA gene: II. The complete nucleotide sequences of 400 mouse KIAA-homologous robnas identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries."; SPECIFICITY.

Dillinger K., W., Liptay S., ARDDINE-222661914; PubMed=12374742; Oswald F., Kostezka U., Astrahantseff K., Bourteele S., Dilling Cowald F., Kostezka U., Astrahantseff K., Bourteele S., Dilling Zechner U., Ludwig L., Wilda M., Hameister H., Knoechel W., Lif Schmid R.M.; anovel component of the Notch/RBP-Ukappa signalling

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                                                                                                                                                       Machine E. The Handan E. Tunnian Fundament D. Furukawa T. Taniguchi Y. Kuroda H., Hamada Y. Toyokuni S., Honjo T.; Taniguchi Y., Kurooka H., Hamada Y. Toyokuni S., Honjo T.; Taniguchi Y., Kurooka H., Hamada Y., Toyokuni S., Honjo T.; Taniguchi Y. Kurooka H., Hamada Y., Toyokuni S., Honjo T.; Taniguchi Y. Kurooka H., Hamada Y., Toyokuni S., Honjo T.; Toyokuni S., Honjo T.; Toyokuni S., Honjo T.; Toyokuni S., Honjo T.; Toyokuni S., Honjo T.; Toyokuni S., Honjo T.; Toyokuni S., Honjo T.; Toyokuni S., Honjo T.; Toyokuni S., Honjo T.; Toyokuni S., Honjo T.; Toyokuni S., Honjo T.; Toyokuni S., Honjo T.; Toyokuni S., Honjo T.; Toyokuni S., Honjo T., Honjo T., Honjo T.; Toyokuni S., Honjo T., Honjo T., Honjo T.; Toyokuni S., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T., Honjo T.,
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Noce-No experimental confirmation available;
Noce-No Experimental confirmation available;
ISSUE SPECIFICITY: Highly expressed in testis. Expressed at lower level in brain, lung, spleen, liver and kidney. Weakly expressed in cardiac and skeletal muscles and ovary. In spleen, it is marginal zone B-cells, while it is weakly expressed in DOMAIN: The RID domain mediates the interaction with nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- DOWALN: The SPOC domain, which mediates the interaction with NCOR2, is essential for the repressive activity (By similarity).
-1- SIMILARITY: Belongs to the Spen family.
-1- SIMILARITY: Contains 1 RID (receptor interacting) domain.
-1- SIMILARITY: Contains 4 RNA recognition motif (RRM) domains.
-1- SIMILARITY: Contains 1 SPOC domain.
-1- SIMILARITY: Contains 6 Spoc domain.
-1- CAUTION: Ref. 4 Sequence differs from that shown due to multiple frameshifts and conflicts that create stop codons.
-1- CAUTION: Ref. 5 Sequence differs from that shown due to what seems to be the presence of intronic sequence in the cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50102; RRM; 4.
PROSITE; PS50102; RRM RNP 1; FALSE_NEG.
PROSITE; PS50917; SPOG; 1.
PROSITE; PS50917; SPOG; 1.
PROSITE; PS50917; SPOG; 1.
RNA-binding; Repeat; Colled coil; Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q62504-1; Sequence=Displayed;
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EMBL, AR156529; AAD55931.1; ALT_INIT.
EMBL, AR055980; BAB32786.1; -.
EMBL; Z78160; CAB01562.1; ALT_SEQ.
EMBL; AK122402; BAC65684.2; ALT_SEQ.
INCEMPC, IRRO056, M.In.
IncerPc, IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 3.
PROMETER SM00360; RRM; 3.
PROMETER SM00360; RRM; 3.
                                                                                                                                        WEDLINE=22483652; PubMed=12594956;
                                                                                                FUNCTION, AND TISSUE SPECIFICITY
pathway.";
EMBO J. 21:5417-5426(2002).
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SSTASDDSPAR------SVQSAAVPAPTSQLLSSLEXDEPRKSFGIK 339
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| 1524 | 1524 | D -> A (IN REF. 3) |
| 1560 | 1560 | H -> Y (IN REF. 3) |
| 1570 | 1570 | F -> L (IN REF. 3) |
| 1571 | 1574 | 1574 | R -> G (IN REF. 3) |
| 1572 | 1574 | G | G -> R (IN REF. 3) |
| 1669 | 1669 | G -> R (IN REF. 3) |
| 1669 | 1669 | G -> R (IN REF. 3) |
| 1669 | 1669 | G -> R (IN REF. 3) |
| 1669 | 1669 | G -> R (IN REF. 3) |
| 1669 | 1669 | G -> R (IN REF. 3) |
| 1669 | 1669 | G -> R (IN REF. 3) |
| 1670 | 1670 | G -> A (IN REF. 3) |
| 1681 | 1682 | G -> A (IN REF. 3) |
| 1682 | 1683 | G -> A (IN REF. 3) |
| 1683 | 1684 | 1684 | 1685 | 1685 |
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DNA-BINDING.
RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 3.
RNA-BINDING (RRM) 3.
RNA-BINDING (RRM) 4.
COLLED COLL (POTENTIAL).
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WITH RBPSUH.
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/FIId=VSP_008564.
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INTERACTION W
ARG-RICH.
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TYR-RICH.
ARG-RICH.
ALA-RICH.
PRO-RICH.
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950	982 SIESYSEDDESKFCSYGQY	1013 HMDDNDGELDTPINYSLKYSDEQLNSGRQSPSQNERWARP :   :   :	1053 KHIIEDEIKQS-EQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQQECVSPYRSR	1106 GANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKPTNYSERYSEE	1151 EQHEEEBRPTNYSIKXNEEKRHUDQPIDYSLKYAIDIPS-SQKQS ::       :: :         ::	1195 FSFSKSSGQSSKSS 1195 FSFSKSSGQSSKSS 1195 FSFSKSSGSSSVSPPRYDKLEKARLERYTKNEKADKERTFDPERVERERRIVRKEKGE	1224 NAKRQNQLHPSSAQSRSGQPQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSLSSA 	EDBIGCNQTTQEADSANTLQIAEIKGKIGTRSAEDPVSEVPAVSQHPRTKSSRL	1338QGSSLSSESARHKAVEFPSGAKSPSKSGAQTP 		THE TRANSPORT TO THE TR	1054 PVRKEILKRESKKTKLERLNSALSPKÖCQDPAAVSAGSGSRPSSDVHAGLGELTHGS 1428 GOTMPPSRSKTPPPPPOTAOTKREVPKNKAPTAEKRESGPKOAAVVGKVOVLPDADT		1488 ILHFATESTPDGFSCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNE	1548 NQEKEAEKTIDSEKDLIDDSDDDIEILEECIISAMPTKSSRKGKKPAQTASKLPPP	1605 VARKPSQLPVXXLLPSQNRLQPQ-KHVSFTPGDDMPRVYCV   :   :	1645 EGTPINFSTATSLSDLTIESP :	1666AQGGKTSS-  1666AQGGKTSS-  1360 KQDPSRFDVSFPNSVIKRDSLRKRSVRDLEPGEVSDSDEDAEHRSQSFRASSF	1708 VTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASAS
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1414	
1757	SSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSK 1796
1797	
1845 1586	HYTPIEGTPYCFSRNDSLSSLDPDDDDVDLSREKAELRKAKENKESE 1891
1892	AKVTSHTELTSNQQSANKTQAIAKQPINRGQPKPILQ 1928 
1929	SVPVEQPRQSDVPPGEDSRDSQNAATDEKLONFALENTPVCFSHN 1966
1967	SSLSSLSDIDQENNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFH 2013
2014	VEDTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPKKKKFPSRLKGDNEKRSP 2065
2066	RNMGGILGEDLTLDLKDLQRP- 
2091	STD
1931	DHESRSPAKEPVEQPRUTRKRLERELQBAVVPPTTPRRGRPPKTRRRAEEDGEHERKEPA 1990
2105	QBGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHL 2150
2151	TPDQEEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITG 2201 
2202	KVRSNSEISGQMKQPLQANMESISRGRIMIHIPGVRNSSSST 2243
2244	
2286	<b>∢</b> —∢
2326	
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2442	TFIKEAPSPTLRRKLEESASFESL
23/4	AATFEAFQBEKFSENFFSFFABCIFUFONIF-FFABSENSMAN 271QAGGWRKIPPNLSPITEYNDGRPAKRHDIARSHSBSP

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Score 417;
Pred. No. 3.
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C2H2-TYPE.
C2H2-TYPE.
POLY-SER.
POLY-PRO.
C2HC-TYPE (
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C2H2-TYPE.
           1169 EKRHVDQPIDYSLKYATDIPS--
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   AAA98810.1;
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2418 KTPCKAPVLPALPPLSQPAL-MDDGPQARFKVHSIIESDPVTPPSDSGIPPPTIPLVTIA 2476
                                                                           2526
                                                                                                                                                -----TSSSTLRKILMDPKYVSATGVTSTAIAAEPVSAPCL--QEAPA 2570
                                                                                                                                                                                    2651 VSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDNQA----- 2702
                                                                                                                                                                                                                        -------PPLEGVSAAAVPN----ADTQASEVPVAAD 2603
                                                                                                                                                                                                                                                             2703 KONVGNGSVPMRTVGLENRLTSFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVERTPF 2762
                                                                                                                                                                                                                                                                                                 2604 KEKVAPVIAP-----KITSVI------SRMPVSIDLENSQKITLAKPA 2640
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                                                                         2477 KLPPPVIPGGV-----PHOSPPFKVTEWITRQEEPRAQSTPSPALPPDTKASDMD----
                                   RL--PINRSGTWKREHSKHSSSLPRVSTW---RRTGSSSSILSASSESSEKAKSEDEKHV
                                                                                                           2593 NSISGTKQSKENQVSAKGTWRKI--KENEFSPTNSTSQTVSSGATNGAESKTLIYQMAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 40 (Transcription factor alphaA-CRYBP1) (Alpha A-CRYSTAILIn-binding protein I) (Alpha A-CRYBP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura T., Donovan D.M., Hamada K., Sax C.M., Norman B., Flanagan J.R., Ozato K., Westphal H., Piatigorsky J., "Regulation of the mouse alpha A-crystallin gene: isolation of a cDNA encoding a protein that binds to a cis sequence motif shared with the major histocompatibility complex class I gene and other genes."; Mol. Cell. Biol. 10:3700-3708(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Nuclear.
-!- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPRATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH ZINC-FINGER IN-BETWERN.
-!- SIMILARITY: STRONG, TO HIVEP2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brady J.P., Kantorow M., Sax C.M., Donovan D.M., Piatigorsky J., "Murine transcription factor alpha A-crystallin binding protein I Complete sequence, gene structure, expression, and functional inhibition via antisense RNA.";
                                                                                                                                                                                                                                                                                                                                     2763 SSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSOIPTPVN 2810
                                                                                                                                                                                                                                                                                                                                                                        2641 PQTLTGLVSALTGLVNVSLVPVNALKGPVKGSVATLKGLVSTPAGPVN 2688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 2688 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95138112; PubMed=7836383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 2024-2688 FROM N.A.
TISSUE-Lens epithelium;
MEDLINE-90287161; PubMed-1694016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1117 SNHGINQNVSQSLCQEDDYEDDKPTNYSERYSE-EEQHEEEERPTNYS-----IKYNE 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- SQKQSFSFSKSSSGQSSKT 1208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 OIHPRN-LRDKIEBAQKELNGAEVSKKEVLBAGVKGTSESLKGVKRKKIVAENHLKKIPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 ETPGMTAESSES----GDLVSPKKTSSPHORSELRRWRSEGSDPTRLSGLDGQRDSSSSS
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PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2688;
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                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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Matches 463; Conservative 323; Mismatches 898;
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The standard of the sassociated protein IA (MAPLA) gene and its assignment to human chromosome 15.";

MAPLA) gene and its assignment to human chromosome 15.";

U. Neurosci. Res. 40:820-825(1995).

-!- PUNCTION: Structural protein involved in the filamentous cross-bridging between microtubules and other skeletal elements.

-!- SUBUNIT: 3 different light chains, LCI, LC2 and LC3, can associate with MAPLA and MAPLB proteins.

-!- SUBUNIT: 3 different light chains, LCI, LC2 and LC3, can associate with MAPLA and MAPLB proteins.

-!- DOMAIN: THe basic region containing the repeats may be responsible containing of MAPLA to microtubules.

-!- DOMAIN: THe basic region containing the phosphorylated by CAMP kinase.

-!- PTM: LC2 IS COEXPRESSED WITH MAPLA. IT IS A POLYPEPTIDE GENERATED COEXPRESSED WITH MAPLA. IT IS A POLYPEPTIDE GENERATED COEXPRESSED WITH MAPLA. IT IS PREB TO ASSOCIATE WITH BOTH MAPLA AND MAPLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch)
                                                                               TISSUE-Ovarian carcinoma;
Chen Z.C., Faddel A., Naftolin F.;
"Identification of a novel protein (PBO) in ovarian carcinoma cells.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Fink J.K., Jones S.M., Esposito C., Wilkowski J.; "Human microtubule-associated protein la (MAPIA) gene: genomic organization, cDNA sequence, and developmental- and tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lotubule associated complex; TAS.

20805 Phosphorylation.

309 496 INS-RICH (BASIC).

415 541 9 X 3 AA REPEATS OF K-K-[DE].

20 422 2.

77 429 3.

433 4.
                                                                                                                                                    TISSUE=Brain;
Ohtani K., Rutherford T., Sakamoto H., Naftolin F.;
Microtubule associated protein 1A (MAP1A) in human brain sequence and physiological role.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                    TISSUE=Fetal muscle;
Chiannilkulchai N., Pasturaud P., Richard I., Auffray C.
                                                                                                                                                                                                                                                                        Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; 138857; 138857.
Genew; HONC:6835; MAPIA.
MIM; 600178; -
GO; GO:0005875; C:microtubule associated complex; TAS.
Microtubule; Repeat; Phosphorylation.
                                                                                                                                                                                                                                                                                                                       MEDLINE=95356255; PubMed=7629894;
                                                                                                                                                                                                                                                                                                SEQUENCE OF 1607-1883 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U38291; AAB41132.1; -.
EMBL; U38292; AAB41133.1; -.
EMBL; AF200415; AAF08305.2; -.
EMBL; U300458; AAD00355.1; -.
EMBL; Z47038; CAA87104.1; -.
EMBL; U14577; AAA81362.1; -.
                                                                                                                                         SEQUENCE OF 78-1687 FROM N.A.
                                                                                                                                                                                                                           SEQUENCE OF 134-419 FROM N.A.
                                                                     SEQUENCE OF 1-1825 FROM N.A.
                                              Genomics 35:577-585(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSLERERGIGLGNYHPATEN----PGTSSKRGLQIST---TAAQIAKVMEEVSAIHTSQE 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTC-----SMP-YAKLE 955
F -> L (IN REF. 1).

VV -> IP (IN REF. 4).

V -> G (IN REF. 4).

V -> G (IN REF. 4).

S -> G (IN REF. 3).

S -> G (IN REF. 3).

K -> O (IN REF. 1).

AK -> ST (IN REF. 1).

A -> S (IN REF. 1).

A -> S (IN REF. 1).

A -> S (IN REF. 1).

A -> S (IN REF. 1).

K -> D (IN REF. 1).

K -> D (IN REF. 1).

K -> D (IN REF. 1).

K -> D (IN REF. 3).

K -> D (IN REF. 3).

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K -> R (IN REF. 1).

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M -> C (IN REF. 3).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   469 LGGL--QAIAELLQVDCEMYGLTNDHYSITLRRYAGMALTN----LTFGDVANKATLCSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   523 KGCMRAL-VAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   582 \cdot ESTLKSVLSALWNLSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 367; Mismatches 1136; Indels 845;
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CRC64;
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18.7%; Pred. No. 1.6e-07;
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551 DTGLGDKPFPLDTABEGPPSTAIGGTPPSVPGLGGEE 587 956 YKRSSNDSLNSVSSNDGYGKRGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMD 1015	DNDGELDTPINYSLKYSDEQLNSGRQSPSQNERWARPXHIIEDEIKQSEQRQSRNQST	1074 TYPVYTESTDDKHLKFQPHFGQQECVSPYRSRGANGSETNRVGSN- 1118	1119HGINQNVSQSLCQEDDYEDDKPTNYSERYSEBEQHEB-BERPTNYSI 1164 123 TTPAGATEHVSYIQDETIPGYSETEQTISDESIHDEPEBRPAPPRFHTSTYDL 775	1165 KYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSKSSGQ 1204	1205 SSKTEHMSSSSENTSTPSSNAKRONQLHPSSAQSRSGQPQKAATCKVSSINQETIGTYCV 1264 :	1265 EDTPICFSRCSSLSSLSSLSBEDGIGCNQTTQEADSANTLQIAEI 1307	1308 KGKIGTRSAED	1348 RHKAVE-FPSGAKSPSKSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFBSRSIASSVQ 1406 11	1407 SEPCSGMVSGIISPSDLPDSPGGTMPPSRSKTPPPPPQTAQTKREVPKNKAPTAEKRE 1464 	1465 SGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSC 1502 	1503SSSLSALS	1529 QENDNGNETESEQPKESNENQEKEAEKTIDSEK	1567 SDDDDIEILEECIISAMPTKSSRKGKKPAQTASKLPPPVARK 1608 	1609 PSQLPVYKLLPSQNRLQPQKHVSFTPGDDMPRVYCVEGTPINF-STATSLSDLTIE 1663 1302 GKYLPGAITSPDEHLLTPDSSFSKSP-ESLPGP-ALEDIAIKWEDKVPGLKDRTSEQKKE 1359	1664 -SPPNEL	1689 TIPTEGRSTDEAQGGKTSSVTIPELDDNKAEGDILAECINSAM-PKGKSHK 1739	1740PFRVKKIMDQVQQASASSSAPNKNQLDGKKKKPTSPVKPIPQNTBYRT 1787 
9 A	8 & 8	දු පු	රු පු	Qy Db	Q Q	8 S	8 8	Q Dp	8 6	දු පු	දු පු	S G	S G		S q	S q	Qy Dp

2366 2300 2359 2114 SLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEE-KPFTSNKG-----P 2165
1915 EREBEGRAEAPDK--SSHXSKVPEARKSHATTEPEQTEPEQREPTPYPDERSFQYADIYE 1972 2320 2196 2413 1890 -SEAKVTSHTELTSNQQSANKTQALAKQPIN---RGQPKPILQKQSTFPQSS----- 1937 1650 WQETSPIRBEPAGEQKELAPAWEDISPEQDNRYWRGREDVALEQDIYWRELSCERKVWFP 1709 1938 KDIPDRÇAA---TDEKLQNFAIENTPVCFSHNSSLSSLSDIDQENNNKENEPIKE--TEP 1992 ::: | :: | | :: | | :: | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | :: | | | :: | | | :: | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | : 1788 RVRKNADSKNNLNAERVFS--DNKDSKKON---LKNNSKDFNDKLPNNEDRVRGSFAFD- 1841 2275 KPSVK-----SELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRP-2247 --LPRPASPALSEGSSSEATTPVI----SSVAERFSPSLEAAEQESGELDPGMEPAAHXL ---SLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEY--2301 WDLTPLSPAP-PASLDLALAPAPSLPGDWGDGILPCHLECSEAATEKPSPFQVPSEDCAA 2416 XGGSGGPPSSASPEVEAGPQGCXTEPRPHRGELSPSFLNPPLPPSIDDRDLSTEEVRLVG -----IQSPGRNSISPGRNGISPP-----NKLSQLPRTSSPSTASTKSSGSGKMSY -----KREHSKRHDIARSHSESPSRLPINRSGTW----KREHSKHSSSLPRVSTWR 2360 NGPTETSPNPPXPAP----AKAENBEAAAXPAWERGAWPEGAERSSRPDTXLSPEQPVCP 2166 RILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQP----LQAN 2367 T-----SPG----ROMSQONLTKOTGLSKNASSIPRSES-ASKGLNOMNNGNGANKK 2090 SPSPKESGRSHWDDSTSDSELEXGAREQAE------KEAQSPSPPHPIPMGSPT 2566 RTGSSSSILSASSE---SSEKAKSEDEKHVNSISGT-------KQSKENQVSA 2414 VELSRMSSTKSSGSESDRSERPVLVRQSTFIKEAPSPTLRRKLEESASFE------SPHHYTPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAELRKAKENKE-2090 HGLS-----PDSEN---FDW-----KAIQEGA---2321 2464 2518 1842

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C2 DOMAIN 1.
C2 DOMAIN 2.
TKPIN -> SKRK (in isoform 2).
/FIId=VSP 003930.
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2.7%; Score 400; DB 1; Le Best Local Similarity 19.9%; Pred. No. 3.3e-07; Matches 387; Conservative 243; Mismatches 765;
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                                                                                                                                        TPFSSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVNNNTKRDSK 2819
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   ------INNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKD 2699
                                                                                                                                                                       2609 AP----GKDKPVSPXRRLXLR---GKRSPTPGKGSXDRVSRXPXRSRSXTSQVTPAEEKD 2661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
-!- SUBCELLULAR LOCATION: Concentrated at presynaptic side of synaptic
                                    2525 ITAEAALDSDEDGDFLPVDKXGGVSGTHHPRPGHDP----PPL-----PQPDXRPS--
                                                                      2700 NQAKQNVGNGSVPMRTVGLENRLTSFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVER
                                                                                                     ------PPRP----DVCMADPEGLSSESGRXERLRXKEKVQGRVGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20170257; PubMed-10707984; Cases-Langhoff C., Voss B., Enster S.D., Chung W.J., Zhai R., Cases-Langhoff C., Voss B., Garner A.M., Kaempf U., Kindler S., Gundelfinger E.D., Garner C.C.; Piccolo, a presynaptic zinc finger protein structurally related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21181819; PubMed=11285225;
Gerber S.H., Garcia J., Rizo J., Suedhof T.C.;
"An unusual C(2) -domain in the active-zone protein piccolo:
implications for Ca(2+) regulation of neurotransmitter release.";
EMBO J. 20:1605-1619(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- FUNCTION: May act as a scaffolding protein involved in the organization of synaptic active zones and in synaptic vesicle trafficking (By similarity)
-1- SUBUNIT: Interacts with Rabacl/Pral, RIMS2 and profilin (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9JKS6-2; Sequence=VSP 003930, VSP 003931,
-!- DOMAIN: C2 domain 1 is involved in binding calcium and phospholipids. Calcium binds with low affinity but with high specificity and induces a large conformational change.
-!- SIMILARITY: Contains 2 C2 domains.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [3]
CALICUM-BINDING ACTIVITY, AND MUTAGENESIS OF ASP-4668; ASP-4674;
VAL-4688; MET-4689; VAL-4690; SER-4691; GLN-4692; ASN-4693 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fenster S.D., Cases-Langhoff C., Gundelfinger B.D., Garner C.C., Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                              09JKS6; 09JLF1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2), AND INTERACTION WITH RABACI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                  5085 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [sold=Q9JKS6-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuron 25:203-214 (2000).
                                                                                                                                                                                                         2820 TDSTESSG 2827
                                                                                                                                                                                                                                              2662 GHSPMSKG 2669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      junctions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=2
                                                                                                                                        2760
                                                                                                                                                                                                                                                                                                                                 PCLO_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bassoon.
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83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1299 ANTLQIAEIKGKIGTRSAEDPV---SEVPAVSQHPRTKSSRLQGS---SLSSESARHKAV 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 VPPAAAESPSWHRKQELDSSQAPQQPGKPPDPGRPTQPGLSKSRTTDTFRSEQKLPGRSP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QN->AA: MODERATE INCREASE IN AFFINITY FOR CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 IPSSOKOSFSFSKSSSGOSSKTEHMSSSSENTSTPSSNAKRONOLHPS--SAQSRSGOPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VM->SS: 10-FOLD INCREASE IN AFFINITY FOR CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STISLKESKSRIDFKEEYKSSMMPGFFSDVNPLSAVSSVVNKFNPFDLISDSEASQEETT
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R GO; GO:004520; E:csynaptic junction; IDA.

R GO; GO:004520; E:calcium ion binding; IDA.

GO; GO:000554; F:calcium don binding; IDA.

GO; GO:000554; F:profilm binding; IDA.

R GO; GO:000554; F:profilm binding; ISA.

R GO; GO:000552; F:profilm binding; ISS.

R GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.

R GO; GO:001008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:000008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; CO:00008; C
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/FIId=VSP 003931.
D->A: COMPLETE LOSS OF CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D->A: COMPLETE LOSS OF CALCIUM-BINDING
AND CALCIUM-DEPENDENT PHOSPHOLIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 X 10 AA TANDEM APPROXIMATE REPEATS · P-A.-K-P-Q-P-Q-P-X. C4-TYPE (POTENTIAL). C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M->S: INCREASED AFFINITY FOR CALCIUM.
VV->SS: 10-FOLD INCREASE IN AFFINITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V->S: SMALL INCREASE IN AFFINITY FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A->S: NO EFFECT ON CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5085;
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Db 1191	1227	2355		Oy 2395 E	1333		DD 13// G		Qy 2568 G		QY 2603 EI : : Db 1540 K			Qy 2718 L	DD 1619 L	Qy 2776 T	Db 1676 T	Qy 2812 N	Db 1736 Q	RESULT 11	ID ANK2 HUMAN AC 001484; 00		DT 28-FEB-200 DE Ankyrin 2	GN ANK2. OS Homo sapie OC Eukarvota;	OC Mammalia; OX NCBI TAXID		RX MEDLINE=91 RA Otto E., K	"Isolati ankyrins	RL J. Cell Bi RN [2]	
-													<del></del>						,				•				- a			<del></del>
246 QAPGTGKPSQQSPAQTPA	1413 MVSGIISPSDLPDSPGQIMPPSRSKTPPPPPQTAQTKREVPKNKAPTAEKRESGPKQ 1469	278 SAKATVQQPGPAKSPAQPAGTGKSPAQPPAKTPGQQAGLEKTSSSQQPGPKS 329	AAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSSLSALSLDEPFIQKDVELR	LAQTPGHGKFPLGPVKSPAQQPGTAKHPAQQPGPQTAAKVPGP	1524 IMPPVQENDNGNETESEQFESNENQEREARILIDSENDLEDUSJUUDI 15.7 373 TKTPAQQSGPG-KTPAQQPGPTKPSPQQPIPAKPQPQQPVATKTQPQQ		420SAPAKPQPQQPAPAKPQPQPTPAKPQPQPPTPAKPQPQPPTATKP 465		466 QPQFFIATRPHHQQPGLAKPSAQQPTKSISQIVIGKFLQFFFIS-AAQIFAQGLSKIICF 544	CONTTELLLHIPEKANFUTCTECQSTVCSLCGFNPPHLTEIKEWLCLNCQMQRALGGDL	1724 LAEGINSAMPKGKSHKPFRVKKIMDQVQQASASSSAPNKNQLDGKK 1769	585 AAAIPSSPQPTPKAATAPTATASKSPVPSQQASPKKEPPSKQDSPKALESKKPPEPKKPP 644		EPKKPPEPKKPPPLVKQPTLHGPTPATAPQLPVAEALPEPAPPKEPSGPLPEQAKAPVGD	IPQNTEYRIKVRKNADSKONIABERVFSDNKDSKKQNLKONSKDFNDKLPNNEDRV	VEPKQPRMTETRADIQSSSTTKPDILSSQVQSQAQVKTASPLKTDSAKPSQSPPPTGEKT	RGSFAFDSPHHY	**************************************	1888 KESEAKVISHTELTSNÜQSANKIQALAKQFINKGQFKFLLGVO	1937 SKDIPDRGAATDEKLONFAIENTPVCFSHNSSLSSLSDIDQENNNKENBPIKETEPPD 1994	870 QPTTPQETVTGKLFGFGASIFSQASNLISTAGQQGPHPQTGPAAPSKQAPTP 921		AAAENLESKPEQAPTAKKTEKDKK	2053 PSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFDWKA 2103 2050	TORGANSTVASTHOAAAAACLSROASSDSDSTLSLKSGISLGSPP	CTECKNOVCNLCGFNPTPHLTBIQEWLCINCQTQRAISGQLGDMGKMPPAPSG-PKASPM	2149HLTPDOBEKPTSNKGPRILKPGEKSTLETKKIESES 2185.	1089 PAPAEPSSOKTPTGTQVKGKKKEAEGKTEAĒĶPVPEKETASĪĒKTPPMVTTDOKLEĒŠĒ- 1147	2186 KGIKGGKKYYKSLITGKVRSNSEISGQMKQPLQANMPSISRGRIMHIP 2234	
QQ Q	ζ	qq	ò	op o	දු දු	λò	QQ	ે જે	a e	<u>수</u> 음	ò	Db .	ογ	đ	ð.	qq	કે ક	g (	දු දු	λõ	QQ	ζō	qq	۲۵ بر دو	3 8	Z a	ờ	qq	8 8	gn

2235 GVRNSSSTSPVSKKGPPLKTPASKSPSEGGTATTSPRGAKPSVKSE  1191	2513 PTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRT   1426 PKKDSEQGPPSRKEHKEKPELVDDLSPRASSDSSESESBENSPLVKTKTSI   2568 GSSSS	RESULT 11  ANK2 HUMAN  DAKZ HUMAN  STANDARD, PRT; 3924 AA.  C 001486;  DT 01-APR-1993 (Rel. 25, Created)  DT 01-APR-1993 (Rel. 25, Created)  DT 01-APR-1993 (Rel. 34, Last sequence update)  DT 28-FEB-2003 (Rel. 41, Last annotation update)  DE Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid).  GN ANK2.  C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi  OC Mammalla; Eutherra; Primates; Catarrhini; Hominidae; Homo.  OC Mammalla; Eutherra; Primates; Catarrhini; Hominidae; Homo.  OX NOEL_TAXID=9606;  RN [1]  RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  RR TISSUE-Brain stem;  RC TISSUE-Br
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EYKRSSND--SLNSVSSNDGYGKRG--QMKPSIESYSEDDESKFCSYGQYPADLAHKIHS 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1011 ANHMODNOGELDIPINYSLKYSDEQLNSG-----RQSPSQ----NERWARPKHIIE 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1118 NHGINQNVSQSLCQEDDYEDDKPTNYSE-----RYSEEEQHEBEERPTNYSIKYNEEKRH 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1614 CVPLPKEQLQTV------QDKAGKKCEALAVGRSSEKEGKDIPPDETQSTQKQHKPSLG 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1173 VDQPIDYSLKYATDIPSSQKQSFSFSKSSGQSSKTEHMSSSSENTSTPSSNAKRQNQLH 1232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1233 PSSAQSRSGQ-----PQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSLSSAEDEI 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               897 IHTSQEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSE--NSNRTCSMPYAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IYTKESESDQEQEDEBID-MTSEKN-----DETESTETSVLKSHLVNEVPVLASPDLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ::: | | ::: | EVSEMKQDLIKMTAILTTDVSDKAGSIKVKELVKAAEEEPGEPF-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----EIVERVKEDLEKVNEILRSGTCTRDESSVQSSRSERGLVEEEWV----IVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1564 DESISEARQKAPLSITEYPC-VEVRIDKSIK-----GKVE----KDSTGLVNYLTDDLNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1058 DEIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQQECVSPYRSRGANGSETNRVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 307; Mismatches 799; Indels 658; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> QFLGKLHLPTAPPPLNEGESLVSRILQLGPPGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing (In isoform 2 and isoform 3).
/FIIdavSP 000268.
6Q -> PE [IN REF. 4).
I -> S (IN REF. 1).
QY -> HA (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.7%; Score 395; DB 1; Length 3924; 19.5%; Pred. No. 3.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             475 476 GQ -> PE TIN REF. 4).

971 J -> S (IN REF. 1).

3581 3582 QY -> HA (IN REF. 1).

3586 J -> Y (IN REF. 1).

3924 AA; 430337 MW; 52AC496C428E29D2 CRC64;
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/FTId=VSP_000267
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DEATH.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isoid=Q01484-3; Sequence=VSP 000268;
-!-TISSUE SPECIFICITY: Plasma membrane of neurons as well as glial cells throughout the brain.
-!- PTM: Phosphorylated at multiple sites by different protein kinases and each phosphorylation event regulates the protein's structure and function (Potential).
-!- SIMILARITY: Contains 23 ANK repeats.
-!- SIMILARITY: Contains 1 death domain.
                                                                                                               regulated
                                                                                                                                                                             SEQUENCE OF 463-495 FROM N.A.
MEDLINE-92009921; PubMed=1833308;
TSE W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
Lux S.E., Ward D.C., Forget B.G.;
"Isolation and chromosomal localization of a novel nonerythroid
                                                                                                                                                                                                                                                                                  Genomics 30.85-866(1991).
-!- FUNCTION: Attach integral membrane proteins to cytoskeletal elements. Also bind to cytoskeletal proteins.
-!- ALTERNATIVE PRODUCTS:
                                                   TISSUE=Brain stem,
MEDLINE=94075409; PubMed=8253844;
Chan W., Kordeli E., Bennett V.;
440-kD ankyrinB: structure of the major developmentally redomain and selective localization in unmyelinated axons.";
J. Cell Biol. 123:1463-1473(1993).
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50017; DEATH DÖMAIN; 1.
Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q01484-2; Sequence=VSP_000267, VSP_000268;
                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=3;
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SWART; SM00005; DEATH; 1.
SWART; SM00218; ZD5; 1.
PROSITE; PS50108; ANK_REPEAT; 20.
PROSITE; PS5017; ANK_REP REGION; 1.
PROSITE; PS5017; DEATH_DOMAIN; 1.
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ANK 2.
ANK 3.
ANK 4.
ANK 6.
                                    FROM N.A. (ISOFORM 1).
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EMBL, X56958; CAA40279.2; -.
EMBL, Z26654; CAB42644.1; -.
EMBL, M37123; AAA62828.1; -.
PIR, S37431; S37431.
HSSP; P42771; 1DC2.
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Interpro; IPR000488; Death.
Interpro; IPR000408; 2U5.
Pfam; PF00023; ank; 24.
Pfam; PF00073; datk; 1.
Pfam; PF00791; ZU5; 1.
PRINTS; PR01415; ANKYRIN.
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MIM; 106410; -.
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Cell Biol. 147:151-162(1999)

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MEDLINE=98290545; PubMed=9628581;
                         SEQUENCE OF 4405-4439 FROM N.A.
                                                               SEQUENCE OF 4405-5147 FROM N.A.
           TISSUE=Brain;
                                                                                       Name=2
                                                                                    Name=1
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EMBL; AC004903; AAD20936.1;
EMBL; AC004886; AAD21783.1;
EMBL; AC004886; AAD21783.1;
EMBL; BC0013304; AAH01304.1;
EMBL; AC004082; AAB97937.1;
PIR; T00634; T00634.
HSSP; P04410; IA25.
Genew; HGNC113406; PCLO.
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                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22386257; PubMed=12477932;

X MEDLINE=22386257; PubMed=12477932;

X Strausberg R.D., Faingold E.A., Graue L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jedan H., Moore T., Max S.I., Wang J., Habieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.

A Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergern E.J., Lu X., Gibbs R.A.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rodriguez A.C., Grimwood J., Schwutz J., Dickson M.C.,

Batterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

A Schnerch A., Schein J., Jones S.J.M., Marra M.A.;

R Schnerch A., Schein J. J., Marra M.A.;

R Schnerch A., Schein J., Jones S.J.M., Marra M.A.;

R Human and mouse cDNA sequences.";

K Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                         "Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:31-39(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: May act as a scaffolding protein involved in the organization of synaptic active zones and in synaptic vesicle trafficking (By similarity).
-!- SUBUNIT: Interacts with Rabacl/Pral, RIMS2 and profilin (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
-!- SUBCELLUDAR LOCATION: Concentrated at the presynaptic side of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q9Y6V0-2; Sequence=VSP 003923, VSP 003924, VSP 003925, VSP 003927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note=No experimental confirmation available;
-!- DCMAIN: C2 domain 1 is involved in binding calcium and phospholipids. Calcium binds with low affinity but with high specificity and induces a large conformational change.
-!- SIMILARITY: Contains 2 C2 domains.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                              Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
                                      SEQUENCE OF 552-4404 FROM N.A.
Kraemer J., Wollam C., Wohldmann P., McGrane B.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kalicki J., Elliott G.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                SEQUENCE OF 3619-5147 FROM N.A. (ISOFORM 2)
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QTGKLMEG (in isoform 2).
/FTId=VSP_003923.
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C4-TYPE (POTENTIAL).
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GO; GO:0045202; C:synaptic junction; ISS.
GO; GO:0045202; C:synaptic junction; ISS.
GO; GO:0005549; F:calcium ion binding; ISS.
GO; GO:0005522; F:profilin binding; ISS.
GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
InterPro; IPR001065; Synaptic vesicle targeting; ISS.
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PRINTS; PRO0399; SYNAPTOTAGMN.
SMART; SM00239; C2; 2.
PROSITE; PS500049; C2_DOMAIN 1; 1.
PROSITE; PS50004; C2_DOMAIN 1; 1.
Repeat; Alternative splicing.
NON_TER
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S-farnesyl cysteine.
K -> N (in dbSNP:7289)
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Local Similarity 17.9%; Pred. No. 6.6e-07;
les 577; Conservative 502; Mismatches 1239;
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PIR; PC4035; PC4035.
Genew; HGNC:1857; CENPF.
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2165 ASSIIESVVPKPEGPVADTVSTDLLISEKDPVKKAKKETGNGII------LE 2210
                                                   V----DAPDOKGTEIXPGONNPV---PVSETNESPIVER---TPFSSSSS---SKHSS- 2772
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-!- FUNCTION: Probably required for kinetochore function, involved in chromosome segregation during mitosis. Interacts with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhu X., Chang K.-H., He D., Mancini M.A., Brinkley W.R., Lee W.-H.;
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centromere/kinetochore targeting, and dimerization.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=55379648; PubMed=7651420; Zhu K., Mancini M.A., Chang K.-H., Liu C.-Y., Chen C.-F., Shan B., Jones D., Yang-Feng T.L., Lee W.-H.; Characterization of a novel 350-kilodalton nuclear phosphoprotein that is specifically involved in mitotic-phase progression."; Mol. Cell. Biol. 15:5017-5029(1995).
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MEDLINE=95336446, PubMed=7612011;
Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., Joshi H.C.,
"A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal
domain sufficient for nuclear localization.",
Biochem. Biophys. Res. Commun. 212:220-228(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-Breast carcinoma;
MEDLINE=95348175; PubMed=7542657;
Liao H., Winkfein R.J., Mack G., Rattner J.B., Yen T.J.;
"CENP-F is a protein of the nuclear matrix that assembles onto kinetcohores at late G2 and is rapidly degraded after mitosis.";
J. Cell Biol. 130:507-518(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98437347; PubMed=9763420; Chan G.K.T., Schaar B.T., Yen T.J.; "Characterization of the kinetochore binding domain of CENP-E rinteractions with the kinetochore proteins CENP-F and hBUBRL."; J. Cell Biol. 143:49-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20459117; PubMed=10852915; Ashar H.R., James L., Gray K., Carr D., Black S., Armstrong L., Bishop W.R., Kirschmeier P.; "Farnesyl transferase inhibitors block the farnesylation of CEN and CENP-F and alter the association of CENP-E with the
                                                                                                                                                                                                                                                                                                                                             CENF HUMAN STANDARD; PRT; 3210 AA.
P49454; Q13171; Q13246;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
CENP-F kinetochore protein (Centromere protein F) (Mitosin)
                                                                                                                                                           2773 -PSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTP 2808
                                                                                                                                                                                                            2271 LÞSGSPSVSSLÞAKPRÞFRSSSLĎ-ISAQÞPPÞÞPP 2306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM, N.A.
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CCCERTERARY REPRESENTARY BUREA

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
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T -> A (IN REF. 2).

G -> D (IN REF. 2).

MISSING (IN REF. 2).

MISSING (IN REF. 2).

MISSING (IN REF. 2).

V -> A (IN REF. 2).

V -> L (IN REF. 2).

ER -> DG (IN REF. 2).

ER -> DG (IN REF. 3).

D -> N (IN REF. 3).

D -> N (IN REF. 3).

EX -> QG (IN REF. 3).

D -> N (IN REF. 2).

ELNERVAALHNDQBACK -> SSWREWQPCIMTKKPVS
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SUBGNIT: Homo- or heterodimer.
SUBCELLULAR LOCATION: Nuclear matrix (but not in the nucleolus),
reorganization to the Kinetochore/centromere (coronal surface of
the outer plate) and the spindle during mitosis.
DEVELOPMENTAL STAGE: Gradually accumulates during the cell cycle.
PTM: Hyperphosphorylated during mitosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKI, P49454; ---
MIM; 600236; --
MIM; 600256; --
GO:0005634; C:kinetochore; TAS.
GO: GO:0005634; C:nucleus; TAS.
GO: GO:0005639; C:spindle; TAS.
GO: GO:000067; P:DNA replication and chromosome cycle; TAS.
GO: GO:0007068; P:regulation of mitosis; TAS.
GO: GO:0007088; P:regulation of mitosis; TAS.
GO: GO:0007089; P:regulation; Muclear protein; Centromere; Coiled coil;
Mitosis; Phosphorylation; Antigen; Cell cycle; Repeat; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 DQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAMASSGQI
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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2 X 177 AA TANDEM REPEATS.
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179 628 231 231 343 343 343 343 343 343 343 343 343 3

1411 FLSLQSEHKILHDQHCQMSSKMSELQTYVDSLKAENLVLSTNLRNFQGDLVKEMQLGLEE 147	1470
1243PQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSLSSLEBIGCNQTTQ 125	
E EADSANTLQ - IAEIKGKIGTRSAEDPVSEVPAVSQHPRTKSSRL 13	
1338 QGSSLSSESARHKAVEFPSGAKSPSKSGAQTPKSP 13'	
1373 PEHYVQETPLMFSRCTSVSSL-DSFESRSIASSVQSEPCSGWVSGIISPSDLPDSPGQTM 14:	1431
1432 PPSRSKTPPPPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDAD 1400	1486
1487 TLLHFATESTPDGFSCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPK-ES 15.	1545
1546 NENGEKEAEKTIDSEKDLLDDSDDDIEILEECIISAMP-TKSSRKCKKPAQTASKLPPP 16( 1. :	1604
1605 VA-RKPSQLPVYKLLPSQNRLQP-QKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTI 16( :	1662
SGEF 1   	1684
1685 EKRDTIFTEGRSTD-EAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKS 17 :::  :  :  :  :  :  :  :  :  :  :  :  :	1737
1738HKPFRVKKINDQVQQASASSSAPNRVQLDGKKKK 17 2009 SIEHEALYLEADLEVVQTEKLCLEKDNENKQKVIVCLEEELSVVTSERNQLRGELDTMSK 20	
1772 PTSFVKPIPQNTEYRTRVRKNADSKNNLANBERVFSDNKDSKKQNLKNNSKDFNDKLPNNE 18	
ESE 1     EKE 2	1891
1892 AKVISHTELTSNQOSANKTQAIAKQPINRGQPKPILQKQSTFPQSSKDIPDRG 19 2163 LLVKESESLQARLSESDYEKLNVSKALEAALVEKGEFALRLSSTQEEVHQLRRGIE 22	1944
1945AATDEKLQNFAIENTPVCFSHNSSL-SSLSDIDQE-NNNKENEPIKETEPPDS 19 2219 KLRVRIEADEKKQLHIAEKLKERERENDSLKDKVENLERELQMSEENQELVILDAENSKA 22	1995
U U	
2050 KKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIORPDSEHGLSPDSENFDWKAIQEGAN 21::::	
2110 SIVSSLHQAAAAACLSRQASSDSDSILSLKKGI-SLGSPFHLTPD 21	2153

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PTM: Phosphorylated.
SIMILARITY: TO MAPIA.
CAUTION: A C-terminal
2387 PPIEEEHQLRNSIEKLRARLEADEKKQLCVLQQLKESEHHADLLKGRVENLERELEIART 2446
                                                                                                                                                 2534
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                                                                                                                                                                                                                                                                                                                                                                2630 QEQLVSKLSQVEGEHQLWKEQNLELRNLTVELEQKIQVLQSKNASLQDTLEVL---0SSY- 2686
                                                                                                                                                                                                                                                                                                                                                                                                     2445 KEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQ--AG 2502
                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KNLENELELTKMDKMSFVEKVNKMTAKETELQREMHEMAQKTAELQEELSG 2737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTQILEELKKTKMDNLKYVNQLKKENE-RAQGKMKLLIKSCKQLEEEKEILQKELSQLO 2916
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                                    QEBKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQM
                                                                                                          2214 KQPLQANMPSISRGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSBGQTATTSPRG
                                                                                                                                                                                                                                                      2334 NGISPPNKLSQLPRISSPSTASTKSSGSKMSYTSPGRQMSQQNLTKOTGLSKNASSIPR
                                                        2274 AKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGR
                                                                                                                                                                                                         AMEMLQTQLKELNBRVAAL-------HNDQEACKAKEQNLSSQVECLELEKA----
                                                                                                                                                                                                                                                                                                                             2394 SESASKGINQM------NNGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQSTFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GNGSVPMRTVGLENRLTSFIQV---DAPDQKGTEIKPGQNNP-----VPVSETNE
                                                                                                                                             2494 TNELOKEOERISELE-----IINSSFENILQEKEQEKVOMKEKSST------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2503 GWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRL-----PINRSGTWKRE----
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P15205; 062958; 095R21; 090W92;
01-APR-1990 (Rel. 14, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) (Neuraxin) (Contains: MAP1 light chain LCl).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---TPVNNNTKKRDSKTDST----ESSGTOSPK 2832
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.

Rattus norvegicus (Rat).

NCBI TaxID=10116:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         postnatal development and are low in adults. In derease during postnatal development and are low in adults. In derease during ganglia levels remain high throughout development.

INDUCTION: By nerve growth factor.

INDUCTION: By nerve growth factor.

INDUCTION: By a highly basic region with many copies of the sequence KKEE and KKEI/V. repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules.

PTM: LCI is coexpressed with MAPIB. It is a polypeptide generated from MAPIB by proceedytic processing. It is free to associate with both MAPIB and MAPIB. It interacts with the amino-terminal region of MAPIB. (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cortex, spinal cord and sciatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAUTION: A C-terminal fragment of this protein (residues 1597 to 2459) was originally described as neuraxin in Ref.3.
                                                                                                                                                                                                                                                                                                          TISSUE-Spinal cord;
MEDILINE-90059811, PubMed=2555150,
Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J.,
Littauer U.Z., Prior P. V., Gundelfinger B.D., Schnitt B., Betz H.;
"Neuraxin, a novel putative structural protein of the rat central nervous system that is immunologically related to microtubule-associated protein 5.";
EMBO J. 8:2879-2888(1989).
                                                                      Liu D., Fischer I.; "Isolation and sequencing of the 5' end of the rat microtubule-associated protein (MAPIB)-encoding cDNA."; Gene 172:307-308(1996).
                                                                                                                                                                                                        . G.;
ing domains c
                                                                                                                                                                                                                                                                                           SEQUENCE OF 1541-2459 FROM N.A., AND TISSUE SPECIFICITY
                                                                                                                                                      SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION. STRAIN-Sprague-Dawley; TISSUE-Brain, and Glial tumor; MEDLINE-92347374; PubMed=1639092;
                                                                                                                                                                                                        Zauner W., Kratz J., Staunton J., Feick P., Wiche G. "Identification of two distinct microtubule binding recombinant rat MAP 1B.";
SEQUENCE OF 1-142 FROM N.A.
SEQUENCE OF 1-142 FROM N.A.
STRAIN=Sprague-Dawley, TISSUE=Testis;
MEDLINE=96257242; PubMed=8666295;
Liu D., Fischer I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heart or muscle.
DEVELOPMENTAL STAGE: In cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, X60370; CAC16162.1; -.
EMBL, X16623; CAA34620.1; ALT_SEQ.
PIR; AS6577; AS6577.
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                                               CFSHNSSLSSLSDIDQENNNKENEPIKETEPPDSQ-GEPSKPQASGYAPKSFHVEDTPVC
                                                              FSRNSSLSSLSIDSEDDLLOECISSAMPKKKKPSRLKGD------NBKHSPRNMGGILG
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  -KDIPDRGAATDEKLQN---FAIENTPV
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T -> S (IN REF. 1).
R -> K (IN REF. 3).
L -> I (IN REF. 3).
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                                                                                                                                                         TISSUE=Brain stem;
MEDLINE=55138209; PubMed=7836469;
MEDLINE=55138209; PubMed=7836469;
Kordeli E., Lambert S., Bennett V.;
"Ankyring. A new ankyrin gene with neural-specific isoforms localized at the axonal initial segment and node of Ranvier.";
J. Biol. Chem. 270:2352-2359(1995).
-: FUNCTION: Membrane-cytoskeleton linker. The neural-specific isoforms may participate in the maintenance/targeting of ion channels and cell adhesion molecules at the nodes of Ranvier and
                                                                                                                                                                                                                                                                                                                       Event-Alternative splicing, Named isoforms=1,
Comment=A number of isoforms are produced;
Name=1; Synonyms=480-kDa isoform;
Isold=012955-1; Sequence=Displayed;
-! TISSUE SPECIFICITY: Expressed in brain and other tissues. Isoform
-! SIMILARITY: Contains 23 ANK repeats.
-! SIMILARITY: Contains 1 death domain.
                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
LF-MAR-2004 (Rel. 43, Last annotation update)
Ankyrin 3 (ANK-3) (Ankyrin G).
                        PRT; 4377 AA.
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                        STANDARD;
                                                                                                      Homo sapiens (Human)
RESULT 15
ANK3 HUMAN
ID ANK3_HUMAN
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GEGASERIEETMSVHDIMKAFOSGRDPSKELAG 2292	NLMANRPAKYKDANIMSPGSSLPSLHVRK	PDVHKSAAETSAQHAEKD-NQMKPKL 2326	QKALEAELDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNT 816	QAEPTEVÍ1RETKKHPEKEMYVYQKDLSRGDINLKÖ 2374	GNMTVLSPYLNTTVLPSSSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKR 876	FLDEKHDA	SQEDRSSGSTT	:	SNIYNFIKSENSNRTCSMPYAKLEYKRSSNDSLNSVSSNDGYGKRGOMKPSIESYSE 988	DDELSELRGE-SYRFAEKMLLSEKLDVSHSDTEESVTDHAGPPSSELQGSDKRSREKIAT 2508	DDESKECSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQ 1035	APKKEILSKIYKDVSENGVGKVSKDEHPDKVTVLHYSGNVSSPKHAMWARFTEDR 2563	LNSGROSPSQNERWARPKHIIEDEIKOSEQROSRNOSTTYPVYTESTDDKHLKFQPHFGQ 1095	DR2DRTVKEABEKLT-EVSQFFRDKTEKLND 2604	QECVSP-YRSRGANGSETNRVGSNHGINQNVSQSLCQEDDXEDDKFINYS 1144	KNGKE			SGQPQKAAT	QSKAPDGPQSGFQLKQSKLSSIRLKFEQGTHAKSKDMSQEDRKSDGQSR 2745	BDTPICFSRCSSLSSAEDEIGCNQTTQEADSANTL	FAREKQQKAIDLPDESVSVQKDFMVLKTKDEHAQ	QIABIKGKIGTRSAEDPVSEVPAVSQHPRTK-SSRLQGSSLSSESARHKAVEFPSGAK 1359 : :	-SGSDNVKKQRTEMSSKAMPDSFSEQQAKDLACHITSDLATR 2844	-SKSGAQTPKSPPBHYVQETPLMFSRCTSVSSLDSFESRSIAS 1403	GPWDKKVFRTWESSGATNNKSQKEXLSHVLVHDVRENHIGHPESKSVDQKNEFMSVTE 2902	ISPSDLSKTPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP		ATESTPDGFSCS	RVADERRMLSSNIPDGFCEQSAFPKHELSQKLSQSSMSKETVET-QHFNSIEDEKVTY 3019		GKESPSSDV	ECIISAMPTKSSRKGKKPAQTASKLPPPVARKPSQLPV		YKLLPSQNRLQPQKHVSFTPGDDMPRVYCVBGTPINFSTATSLSDLTIESPPN 1667
2260G		2293 LFEHKSAVS	757 QKALEAELDAQI	2327 ERIIBVHIEKGNQAEPTEVÍ	817 GNMTVLSPYLN	2375	877 GLQISTTAAQI	:    : 2396 ELTAEES	932 SNTYNFTKSEN	: : :   2450 DDELSELRGE-,	989 DDESKFCSY	2509 APKKEILSKIY	1036 LNSGRQSPSQN	2564 LDRGREKLIYEDR-	1096 QECVSP-YRSR	2605 - ELQSPEKKARPKNGKE	1145BRYSEEEQH : : :	2641 ASNDEWVKARO	1193 OSFSFSKSSSG	2697 ÓSKAPDGPQSG	1249 CKVSSINQETI	2746 IPVKKÍQESKLPVÝQV	1303 QIAEIKGKIGT : :	2800 VVND	1360 SP	2845 GPWDKKVFRTW	1404 SVQSEPCSGMVSGI	2903 RERKLLINGSI	1444 OTAQTKREVPR	2963 RVADERRMLSS	1504 SSLSALSLDE	3020 SEISKVŠKHQSYV			1615 YKLLPSONRL(  :: : 3115 KKTISORCKTV
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1668	ELAAGEGVRGGAQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELD 1714
1715	DNKAEEGDILAECINSAMFKGKSHKPFRVKKIMDQVQQASASSSAPNK- 1762 
1763	NQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNINAER 1803
1804	VFSDNKDSKKQNLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEG 1851   :   :     :     :
1852 3395	TPYCFSRNDSLSSLDFDDDDVDLSREKAELR-KAKENKESEAKVTSHTEL 1900 
1901	TSNQQSANKTQAIAKQPINRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFALEN 1958   :
1959	
1990	TEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSID 2033  :
2034	-SEDDLLOECISSAMPKKKRPSRLKGDNEKHSPRNMGGILGEDLTLDLKD 2082 
2083	IQRPDSEHGLS-PDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSG 2141 ::
2142	ISLGSPFHLTPDQEEKPTSNKG
2174	NENNNNLDSSTIQTDNIMSNIVLTEHSAPTCTTEKDNPVKVSSGKKTGVLQGHCVRD 3842
3843	NSEISGOMKOPLOANMPSISRGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPAS 2258
2259 3888	KSPSEGGTATISPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLS 2318
2319	RPIGSPGRNSISPGRNGISPPNKLSQLPRTSSPSTASTKSSGSGKMS 2365
3366	YISPGROMSQNLTKOTGLS-KNASSIPR-SESASKGLNOMNGANKKVELSR 2418
2419	MSSTKSSGSESDRSERPVLVRQSTFIKEAPSPTIRRKLEBSASFESLSPSSRPASP-TRS 2477 :
2478	QAQTPVLSPSLPDMSLSTHSSVQAGGRRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPS 2537

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2824 ESSGTQSPKRHSGS 2837

4339 PRLSLHEEEGSSGS 4352

Search completed: August 25, 2004, 17:16:32 Job time : 76.5 secs

Scoring table:

Searched:

Minimum DB 8 Maximum DB 8

Database

Perfect score:

Run on:

Sequence:

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Q8vq99 staphylococ
Q9v736 drosophila
Q8nuj3 staphylococ
Q9uq35 homo sapien
Q99qv4 staphylococ
Q8ifK6 caenorhabdi
Q21227 caenorhabdi
Q21237 caenorhabdi
Q7za38 ashbya goss
Q8ifK6 caenorhabdi
Q7za38 ashbya goss
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Q7xxn1 oryza sativ
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Q9vh10 drosophila
Q9v7g8 drosophila
Q9km1d drosophila
Q9kwr3 streptococc
Q939n5 streptococc
Q9fnd5 arabidopsis
Q8ir22 drosophila
Q9w596 drosophila
O76891 drosophila
Q8cmu7 staphylococ
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Q9vtn2 drosophila
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Vleminckx K., Wong B., Guger K., Gumbiner B.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U64442; AAB4171.1;
InterPro; IPR008938; ARM.
InterPro; IPR001225; Armadillo.
Pfam; PF00514; Armadillo.
SMART; SM00185; ARM; 5.
SEQUENCE 2829 AA; 310878 MW; BA2BABDB7706E496 CRC64;
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Pest Local Similarity 74.3%; Pred. No. 0;
Matches 2128; Conservative 263; Mismatches 416; Indels
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                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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	181 QTDLTRRQLEYEARQIRVAMBEQLGTCODMEKRAQRRIARIQQIEKDILRIRQLLQSQAT 240 181 QTDMTRRQLEYEARQIRAAMBEQLGTCQDMEKRAQRRVGXLHQIEBEILRIRQLLQSQVA 240	241 E-AERSQNKHETGSHDAERQNEGQGVGEINMATS-GNGQGSTTEMDHETASVLSSSSTH 29 [	299 SAPRRITSHIGTKVENVYSLISNIGTHDKDDMSRTLLAMSSSOBSCISNROSGCLPLLIO 3	359 LLHGNDKDSVLLGNSRGSKEARASAALHNIHSQPDDKRGRREIRVLHLLEQIRAYCE 41	419 TCWEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVIMKLSFDEEHRHAMNELGGLQAIAEL 478	479 LQVDCEMYGLTNDHYSITLRRYAGMALTNLFFGDVANKATLCSMKGCMRALVAQLKSESE 5 	539 DLQQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALMNLSAH 598 	599 CTENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRE 658 	659	719 AMGSAALRNIMANRPAKYKDANIMSPGSSLPSLHVRKOKALEAELDAQHISETFDNIDN 778 	779 LSPKASHRSKQRHKQSLYGDTWRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSS 836      :  :      :     :	837 SRGSLDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKR-GLQISTTAAQIAKVMEEVS 895   ::	8 — B	10	1016 DNDGELDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHIIEDEIKQSEQRQSRNQSTTY 1075	1076 PVYTESTDDKHLKFQPHFGQQECVSPY-RSRGANGS-ETNRVGSNHGINQNVSQSLCQED 1133 1076 SSYTENKEEKHKKPPPHFNQSENVPAYTRSRGANNQVDQSRVSSNLSNNSKASKPHCQVD 1135	1134 DYEDDKPINYSERYSEEGHEEE-ERPINYSIK-YNEEKRHVDQPIDYSLKYATDIPSS- 1190   :     :	1 OKOSFSFSKSSGGOSKTEHMSSSENTSTPSSNAKRONQLHPSSAQSRSGOPOKAAT 124	Jo Krest i jannoonkrekkeuvono-ni fi formonkunumanaanookuskeunkrekuten
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Mus musculus (Mouse).
Mus musculus (Motazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Adenomatosis polyposis coli (Fragment)
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Best Local Similarity 94.9
Matches 1004; Conservative 841 196 719 779 839 901 179 239 299 361 421 419 479 541 539 601 599 661 629 721 781 899 959 241 301 359 481 qq ద 9 & 9 19 & 19 Š 엄청 g & ŏ ద δ ò ઠે g 8 8 ò g ð 셤 à 원 원 8 g ò

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LT 3	λŏ	352 CLPLLIQLLHGNDKDSVLLGNSRGSKEARARASAALHNIHSQPDDKRGRREIRVLH 408
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obgoing MRDINNE-99147086; PubMed=10021369; Wetering M., Molenaar M., Wirkpartick C., van de Wetering M., Molenaar M., Mirkpartick C., van de Wetering M., Clevers H.; Miles A., Kuipers J., Destree O., Peifer M., Clevers H.; "Identification of APC2, a homologue of the adenomatous polyposis coli	8 & B	487 IVAQLGSESEELHQVVSSILRNLSWRADINSKKVLREVGSMTALMECVLRASKESTLKSV 546 589 LSALWNLSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIAT 648 [
Curr. Biol. 9:105-108(1999). EMBL; AJ130783; CAA10207.1; EMBL; AJ130784; CAA10207.1; JOINED.	රු අ	649 NEDHRQILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDWGAVSMLK 708   -  -  -  -
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AU130789; CAA10207.1; AU130790; CAA10207.1; AU130791; CAA10207.1; AU130792; CAA10207.1;	Qy qq	768 HLSETFDNIDNLS-PKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMT- 820 
EMBL; AJ130794; CAAL0207.1; JOINED. EMBL; AJ130795; CAAL0207.1; JOINED. EMBL; AJ130795; CAAL0207.1; JOINED. EMBL; AJ130796; CAAL0207.1; JOINED.	S da	821VLSPYLNTTVLPSSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATENPGTSS 874 18
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24.1%; Score 3508.5; DB 11; imilarity 34.4%; Pred. No. 2e-164; Conservative 35.6 Mismatches 789.	λ O	993 KFCSYGOYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNSGROSPSQNERWARP 1052
4 ASYDOLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDBAMA 6	\$ <b>9</b>	1053 KHIIEDEIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQQECVSPYRSRGANGSET 1112
	& A	1113 NRVGSNHGINQNVSQSLCQEDDYEDDKPTNYSERYSEEEQHEEEERPTNYSIKYNEEKRH 1172
	à a	1173 VDQPIDYSLKYATDIPSSQKQSFSFSKSSGQSSKTEHMSSSSENTSTPSSNAKRQNQLH 1232   ::  ::   1014
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LLOSQATEAERSSQNXHETGSHDAERQNEGQGVGEINMATSGNGQGSTTRMDHETASV	Qy Gp	1293 TQEADSANTLQIAEIKGKIGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLS 1343 :     :

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1344 SESARHKAVEFPSGAKSPSKSGAQTPKSPPHYYQETPLMFSRCTSVSSLDSFESRSIAS 1403	1404 SVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQTAQTKREVPKNKA 1457 	1458 PTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSLSALSLDEPFIQ 1517	1518 KDVELRIMPPV-QENDNGNETESEQPKESNENQEKEAEKTIDSEKDLLDDSDDDDIE 1573	1574 ILEECIISAMPTKSSRKGKKPAQTASKLPPPVARKPSOLPVYKLLPSQNRLQPQKHVSFT 1633	1634 PGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQSGEFEKRDIIPTE 1693	1694 GRSTDBAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQA 1753 	1754 SASSSAPNKNOLDGKKKKPTSPVKPIPQNTEY-RTRVRKNADSKNNLNAERVFSDNKDSK 1812 	1813 KONLKANSKDFNDKLPNNEDRVRGSFAFDSPHYTPIEGTPYCFSRNDSLSSLDFDDDV 1872 	1873 DLSREKAELRKAKENKESEAKVTSHTELTSNQOSANKTQAIAKQPINRGQP 1923 	924 KPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSH :       :     :     :       :	984 NEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQECI 2	SSAMPSSAMPSAMPGS	PDSENPDWKALQEGANSIVSSLHQAAAAACLSR( 		SCOMKOPLOANMESISRCRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGOTATT	SPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSI	SPGRNGISPPNKLSQLPRTSSP	1 QTGLSKWASSIPRSESASKGLNOMNGNGA-NKKVELSRMSSTK 242
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2599 KOSKENQVSAKGTWRKIKENEFS-----PTNSTSQTVSSGATNGAESKTLIYQMAPAV 

2115

2652 SKTEDVWYRIEDCPINNPRSGRSPT--GNTPPVIDSVSEKANPNIKDSKDNQAKONVGNG 2709

2710 SVPMRTVGLENRLISFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVERTPFSSSSSK 2769 

HSSPSGTVAARVTPFNYNPSPRKSS--ADSTSARPSQIPTPVN 2810

2770

2154 RKTSDAVVQTEDVATSKTNSSTSPSLESRDPP-----A

1891 QHKTQKSPVRIPEMQRPARRVPPPLARPSPEPGSRGRAGAEGTPGARGSRLGLVRYASAR 1950

2484 L---SPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLP 2541 INRSGTWKREHSKHSSSLPRVSTWRRTGSSSSLLSASSESSEKAKSEDEKHVNSIS--GT

2424 SSGSESDRSERPVLVRQSTFIXEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQTPV

RN [2]

RP SEQUENCE FROM N.A.

RX TISSUB-BATAGE

RX MEDLINE=9944663; PubMed=9823329;

RA Atyama T., Nakamura Y.;

RA Jayama H., Murata Y., Koyama K., Fujiyama A., Miyoshi Y., Monden M.,

RA Jayama T., Nakamura Y.;

RT "Identification of a brain-specific APC homologue, APCL, and its

RT interaction with beta-catenin...;

RT Cancer Res. 58:277-6-181 (1998).

RE FREL, AB022529; BAA74469.1; JOINED.

DR EMBL, AB022521; BAA74669.1; JOINED.

DR EMBL, AB022521; BAA74669.1; JOINED.

DR EMBL, AB022521; BAA74669.1; JOINED.

DR EMBL, AB022522; BAA74669.1; JOINED.

DR EMBL, AB022524; BAA74669.1; JOINED.

DR EMBL, AB022524; BAA74669.1; JOINED.

DR EMBL, AB022525; BAA74669.1; JOINED.

DR EMBL, AB022525; BAA74669.1; JOINED.

DR EMBL, AB022525; BAA74669.1; JOINED.

DR EMBL, AB022526; BAA74669.1; JOINED.

DR EMBL, AB022526; BAA74669.1; JOINED.

DR EMBL, AB022526; BAA74669.1; JOINED.

DR EMBL, AB022527; BAA75469.1; JOINED.

DR EMBL, AB022526; BAA75469.1; JOINED.

DR EMBL, AB022526; BAA75469.1; JOINED.

DR EMBL, AB022526; BAA75469.1; JOINED.

DR EMBL, AB022526; BAA75469.1; JOINED.

DR EMBL, AB022526; BAA75469.1; JOINED.

DR EMBL, AB022526; BAA75469.1; JOINED.

DR EMBL, AB022526; BAA75469.1; JOINED.

DR EMBL, AB022527; BAA75469.1; JOINED.

DR EMBL, AB022526; BAA75469.1; JOINED.

DR EMBL, AB022526; BAA75469.1; JOINED.

DR EMBL, AB022526; BAA75469.1; JOINED. 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
APCL.
APCL.
APCL.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 2231 HGSPSR--AARVPPFNYVPSPMAAATMASDSAVEKAPVSSPAS 2271 Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases 2303 AA Koyama K., Nakagawa H., Nakamura Y.; "APCL exon14."; PRELIMINARY; SEQUENCE FROM N.A. 095996; 4 

GO; GO:0008013; F:beta-catenin binding; TAS.	व्व	PAALSLFLGSPFLQGQALARTPPTRRGGKBAEKDTSGBAAVA
007165; Fisugmai transduction; TAS. FR008938; ARM. ); IPR000225; Armadillo.	کې م م	874 SKRGLOISTTAAOJAKWMESVAAIHTSODDRESGSTTELHCVTDERNALRRSAAHHTS- 932 
; IPR001818; Pept_M10A_M12B. 00514; Armadilo_seg; 3.	ò	933 -NTYNFTKSENSNRTCSMPYAKLEYKRSSNDSLNSVSSNDGYGKRGOMKPSIESYSEDDE 991
100185; ARM; 5. PS00546; CYSTEINE SWITCH; 1. 2303 AA; 243346 MW; 7BF940183ACD643D CRC64;	qu	895 CRGPEGGRREAGSRAHPLIRIKAAHASLSNDSLNSGSASDGYCPREHM942
23.4%; Score 3414.5; DB 4; Length 2303; imilarity 34.3%; Pred. No. 9e-160;	8.8	992 SKFCSYGQYPADLAHKIHSANHMDDNDGBLDTPINYSLKYSDBQLASGRQSPSQNBRWAR 1051
/; Conservative 374; Mismatches 810; Indels 723; Gaps 97; AAASYDOLLKOVEALKMENSNIROELEDNSNHITKLETERASNMKENTKOLOGGTEDEA 59	ò	1052 PXHIIEDEIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQQECVSPYRSRGANGSE 1111
<b>&gt;</b>	qq	RCGQPRPSR
MASSGQIDLLERLKELNLDSSNFPGVKLRSKWSLRSYGSREGSVSSRSGECSPVPMGSFP	8 8	1112 TNRVGSNHGINQNVSQSLCQEDDYBEDKTNYSERYSEEBERPEEERPTNYSIKYNEEKR 1171 967
64 LVSSGQTEVLEQLKALQMDITSLYNLKFQPPTLGPEPAARTPEGSPV-HGSGP 115 20 RR-GFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTE-N 177	8 8	HVDQPIDYSLKYATDIPSSQKQSFSFSKSSGQSSKTEHMSSSSENTSTPSSNAKRQNQL
KDSFGELSRATIRLLEELDRERGFLLNEIEKEEKEKLWYYSQLGGLSKRLDELPHVETQ	8 &	1001 HV
178 FSLQTDLTRRQLEYPARQIRVAMEGLGTCQDMEXRACRIARIOQIEKDILRIRQLLGS 237 [ - - - - - - - - - - - - - - - - - - -	දැ	1032PADHLSKVPEKLAAAPL-SVASKALQKLAAQEGPLSLSRCSSLSSA-GRPGPSE 1086
QATEAERSSQNKHETGSHDAERQNEGQGGGUNMATSGNGQGSTTRMDHETASVLSSSST	ð í	1292 TTQEADSANTLQIAEIKGKIGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSS 1344
PTHPE	3 &	GGULUUSUSSULBGILEFANGESEABLUSINKARIGALSULFVALFAFRKANGRGILGV 1.15 ESARHKAVEFPSGAKSPSKSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFESRSIASS 140
HSARRITSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLI 357 	d d	
LEQIR	ò a	1405 VQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQTAQTKREVPKNKAPTAEK 1462 :
QILHGIEAAAGGKAGARGAPGAKDAKMKANAALHNIVFSQPDQGLAKKEMKVLHVLEQIR 378 AYÇETÇWEWQEAHEPGMD-QDKNPMPAPVEHQIÇPAVÇVLMKLSFDEEHRHAMNELGGLQ 473	ò	RESGEKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSGSSSLSALSLDBFIQKD
	යි දි	
AIAELLQVDCEMYGLTNDHYSITLRRYAGNALTNLTFGDVANKATLCSMKGCWRALVAQL 533  -	à q	
LSALW	À a	1580 ISAMPTKSSRKGKKPAQTASKLPPPVARKPSQLPVYKLLPSQNRLQPQKHVSFTPGDDMP 1639
	පු දු	1640 RVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQSGEFEKRDTIPTEGRSTDE 1699 1389 CTDSAEGTPVNFSSAASLSDETLQGPPRDQPGGPAGRQRPTGRPTSA 1435
NLSAHSTENKAAICQVDGALGFLVSTLTYKCQSNSLAIIESGGGILRNVSSLVATREDYR 618 QILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQBALWDMGAVSMLKNLIHS 713	<u>ک</u> ک	1700 AQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSA 1759
QVIRDHNCLQTLLQHLISHSLTIVSNACGTLMNLSARSARDQBLLMDLGAVGMLRNLVHS 678 KHKMIAMGGAAIDHIMANDDAKYK-DANIMGDGGIDGIHNDKOKRIBARDIDAOHIGET 772	8	PNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLNAERVFSDNKD
	q <sub>Q</sub>	AEQSRGAGKNRAGLELPLGRPPSAPADKD
	y do	1811 SKKONLKNNSKDFNDKLPNNEDRYRGSFPDSPHYTYPIEGTPKSRNDSLSSLDFDDD 1870 1801 GSKPGRTRGDGALOSLCLTTPTEBAVYCFYGNDS 1514
DEHLEKQUEPRARAATIKKELEPLKHLUGLAQDYASUSGCEDDDDAFSSLAAAAATGEFAS 798	ò	1871 DVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQALAKQPINRGQPKPILQKQ 1930

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Best Local Similarity 92.8%
Matches 440; Conservative
Adenomatosis polyposis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDCPINNPRSGRSPTGNT--PPVIDSVSEKANPNIKDSKDNQAKQNVGNGSVPMRTVGLE 2719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2230 ------VDGPSLA-----KAPIS----APFVHEGLGVAVGGFPASRHGSPSR- 2266
                                                                                                                                                                                                                                                                                                                                                                   2436 VLVRQSTFIKEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLST 2495
                                                                                                                                                                                                                                                                                                                                                                                                        HSSVQ-----AGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTW 2547
                                                                                                                                                                                                                                                                                                                                                                                                                                               KREHSKHSSSLPRVSTWRRIGSSSSILSASSESSEKAKSEDEKHVNSISGIKQSKENQVS 2607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKG-TWRKIKENEF----SPINSTSQTVSSGAINGAESKTLIYQMAPAVSKTEDVWVRI 2661
                                                                   1639
                                                                                                                                                                                                                      ---PIQSPGRNSISPGRNGISPPNKLSQLPRTSSPSTASTKSSGSGKMSYTSPGRQMSQQ 2376
                                                                                                                                                                                                                                                                                                  KKKP-SRIKGDNEKHSPRNMGGILGEDLILDLKDIORP----DSEHG-----LSPDSEN 2098
                                                                                                         1683
                                                                                                                          2099 FDWKAIQEGANSIVSSIHQAAAAACLSRQASSDSDSILSLKSGISLGS----PFHLTPDQ 2154
                                                                                                                                        1684 VEWRAIQEGANSIVTWLHQAAA---TREASSESDSILSFVSGLSVGSTLQPPKHRKGRQ 1740
                                                                                                                                                                   2155 EEKPPTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMK 2214
                                                                                                                                                                                    AEGEMGSARRP-----EKRGAASVKTSGSPRSPAGPEK-------PRGT 1777
                                                                                                                                                                                                                                               PSEGQTATTS-PRGAKPSVXSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSR 2319
                                                                                                                                                                                                                                                                  PSPGQQRSRSLHRPAKTSELATISQPPRSATPPARLAKTPSSSSSQTS----PASQPLPR 1888
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                                                            SEPPAVHPRGREPAVT-----KDPGPGGGRDSSPSP---RAABEBLQRCISSALPR
                                                                                                    2377 NLTKOTGLSKNASSIPRSESASKGLNOMNNGNGA-NKKVELSRMSSTKSSGSESDRSERP
           STFPQSSKDIPDRGAATDEKLQ-NFAIENTPVCFSHNSSLSSLSDIDQENNNKENEPIKE
                                                                                                                                                                                                         OPLOANMPSISRGRIMIHI-------PGVRNSSSSTSPVSKKGPPLKTPA--SKS
                                                 TEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPK
                       KEAPAPSKAAP--AAPPPARTQPSLIADETPPCYSLSSSASSLS-
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15.3%; Score 2229; DB 11; 92.8%; Pred. No. 3.8e-102; ive 12; Mismatches 20;

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-ISGQIDLLERLKEFNLD-SNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR

61

1 MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDETM 61 ASSGOIDLIERLKEINLDSSNFPGVKLRSKMSIRSYGSREGSVSSRSGECSPVPMGSFPR

MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLFTEASNMKEVLKQLQGSIEDEAM

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300
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                       EAERSSQNKHETGSHDAERQNEGQGVGEINWATSGNGQGSTTRMDHETASVLSSSSTHSA
                                                                                                                                   HONDKDSVLLGNSRGSKEARARARAALHNIIHSQPDDKRGRREIRVLHLEQIRAYCETC
                                                          QTDLTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT
                                                                                                                                                                            PRRLISHLGTKVEMVYSLLSMLGTHDKDDMSRTLLLAMSSSQDSCISMRQSGCLPLLIQLL
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RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
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(TrEMBLrel. 23, C (TrEMBLrel. 23, I (TrEMBLrel. 25, I

Q8BRD8; Q8BRD8; 01-MAR-2003 ( 01-MAR-2003 ( 01-OCT-2003 (

RESULT OBBRD8 ID O8 AC O8 DT 01 DT 01

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PRELIMINARY;

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LSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGTLRNVSSLIATNEDHRQ
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01-NOV-1999 (TrEMBLrel. 12,
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MEDLINES-99147086; PubMed=10021369;
WEDLINES-99147086; PubMed=10021369;
van Es J.H., Kirkpatrick C., van de Wetering M., Molenaar M.,
Miles A., Kuipers J., Destree O., Peifer M., Clevers H.,
"Identification of APC2, a homologue of the adenomatous polyposis coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLOTDLTRROLEYBAROIRVAMBEQLGTCQDMEKRAQRRIARIQQIBKDILRIRQLLQSQ
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                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 733;
                                                                                                                                                                                                                                                                                                                                                         Miles A., Kirkpatrick C., van de Wetering M., Molenaar M., Miles A., Kuipers J., Destree O., Peifer M., Clevers H.; "Adenomatous Polyposis Coli Homologs in Mammals and Flies."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AJ012652; CAB61207.1; -... EMBL, AJ012652; AAF01784.1; -... InterPro; PRRO08298; ARW. InterPro; IPR000225; Armadillo. Pfam.; PF00514; Armadillo. Pfam.; PF00514; Armadillo. Seg; 3. SNART; SMO0185; ARM; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
14.9%; Score 2172.5; DB 4; Length
Best Local Similarity 57.6%; Pred. No. 4e-99;
Matches 446; Conservative 121; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80876 MW; 09E56BE5F7032BAD CRC64;
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  protein (Fragment)
                                        sapiens (Human)
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              tumour suppressor
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                                                                                                        NCBI_TaxID=9606;
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41; 654 714 60 MASSGQIDLLERLKEINLDSSNFPGVKLRSKWSLRSYGSREGSVSSRSGECSPVPMGSFP 119 238 120 RR-GFVNGSRESTGYLEELEKERSLILADLDKEEKEKDWYYAQLONLTKRIDSLPLTENF 178 299 SAPRRITSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQ 358 4 SVAPYEQLVRQVEALKAENSHLRQELRDNSSHLSKLETETSGMKEVLKHLQGKLEQEARV 63 Carr I.M., Markham A.F., Colleta P.L., Wai L., Askham J., Morrison E., Mardith D.M.; Markham A.F., Colleta P.L., Wai L., Askham J., Morrison E., Meredith D.M.; Marchatvely spliced cDNA sequence.";

"APC2 alternatively spliced cDNA sequence.";

"Marchited (NOV-1998) to the EMBL/GenBank/DDBJ databases.

"BMBL; AF110334; AAD28183.1; -..

"BMBL; AF110334; AAD28183.1; -..

"BMSC; QO:00005278; C:extracellular matrix; IEA.

"GO; GO:0004222; F:metalloendopeptidase activity; IEA.

"GO; GO:0004222; F:metalloendopeptidase activity; IEA.

"GO; GO:0004222; F:metalloendopeptidase activity; IEA.

"GO; GO:0004222; F:metalloendopeptidase activity; IEA.

"GO; GO:0004222; F:metalloendopeptidase activity; IEA.

"GO; GO:000508; P:proteolysis and peptidolysis; IEA.

"InterPro; IPR001818; Pept MIOA M12B.

"R Pfam; PR00184; Armadillo\_seg; 3.

"R PART; SM00185; ARM; 3.

"R PART; SM00185; ARM; 3.

"T NON TER.

"ACCOUNTY OF THE TOTAL OF THE . Ш ILRENNCLOTILIOHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSK 2 AAASYDQLLKQVEALKWENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEA--64 LVSSGQTEVLEQLKALQMDITSLYNLKFQPP----TLGPEP---AARTPEGSPV-HGSGP 179 SLQTDLTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQ 239 ATEAERSSONKHETGSHDAERQNEGQGVGEINMATSGNGQGSTTRMDHETASVLSSSSTH Gaps HKMIAMGSAAALRNIMANRPAKYK-DANIMSPGSSLPSIHVRKQKALEAELDAQ 767 Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606; 13.7%; Score 1989.5; DB 4; Length 1246; larity 30.5%; Pred. No. 9e-90; Conservative 194; Mismatches 428; Indels 697; 1246 AA; 132115 MW; 8C527DA2B3B0BC17 CRC64; Last sequence update) Last annotation update)

us-09-442-489f-2.rspt

vacive 330; TGSHDAERQN-EGÇ	1355 PSGAKSPSKSGAQIPKSPPEHYVQETPIMFSRTISVSSLOSFESRSIASSVOSEFUSGMV 1414  B68TPSSSSENYVQETPIVASRCSSVSIGSFESPSIASSIPSEPSGHG 914	& g
O1 10	:: :   :: :   DSSLEGLEBAGPIEAELDSTWRAPGATSLPVAIPAPRRNRGRGLGVEDA	qa
	ANTLOIAEIKGKIGTRSAEDPVSEVPAVSQHPRTKSSRLOGSSLSSESARHKAVEF	ò
DR Phen, PRO0514, Armadillo. DR Phen, PRO0514, Armadillo. DR Phen, PRO0514, Armadillo. DR Phen, Professor Armadillo.	1239 RSGOPOKAATCKVSSINGETIOTYCVEDTPICFSRCSSISSLSSAEDEIGCNOTTOEADS 1298	ð
DR GO; GO:0008013; F:beta_catenin binding; I	11/9 ISLETINDEDENGORDENGOSONIERUSSSSENISIEROKANKULIERUSSKY LILIS 12. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	£ 5
RL Proc. Natl. Acad. Sci. U.S.A. 94:242-247 DR EMBL; U7947; A5811404:1;	TDLDPPGCQAEPPAREATSADARVRTIKLSPTYQHV 727	අුර (
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RP SEQUENCE FROM N.A.  RX MEDLINE=9714445. Pubmed=8990193;  DA HANAEN'S ENHYNFEIG R. SONYA R. POLBA	1059 BIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQQECVSPYRSRGANGSETNRVGSN 1118	ò
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	92) KKEAGSKARFLEKKAKARASUSNUSSKASUGICKKERM	3 8
	KSENONRTCSMPYAKLBYKRSSNDSINSVSSNDGYGKRGGMKPSIESYSEDDESKFCSYG 9	8
DT 01-MAY-1997 (TrEMBLrel. 03, Created) DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation)	881 STTAAQIAKVMEBVSAIHTSQEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFT 938 :  - - - - - - - - - - -	oy Ob
RESULT 8 P91667 ID P91667 PRELIMINARY; PRT; 2416	824 PYLNTTVLPSSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQI 880 :	S S
	778 NLSPKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLS 823	Sy do
1195	719 AMGSAAALRNLMANRPAKYK-DANIMSPGSSIPSLHVRKQKALBAELDAQHLSETFDNID 777 	ò a
	659 NNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQBALWDWGAVSNLKNLHSKHKMI 718 	\$ 8 8
1123	599 CTENKADICAVDGALAFLYGTLITYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRE 658	γς G
1082	539 DLQQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWNLSAH 598 :    :: :	장 원
1027	479 LQVDCEMYGLTNDHYSITLRRYAGNALINLTFGDVANKATLCSMKGCMRALVAGLKSESE 538        - :     - :	B S
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1473	16	qa
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.5; DB 5; Length 2416;
5.8e-79;
hes 845; Indels 935; Gaps 101;
                                                   SCSSSLSALSLDEPFIQKDVELRIMPPVQ 1529
                                                                                                                                                                                                             )SGEFEKRDTIFTEGRST----DEAQGGKT 1705
|----QRPTGRFTSARQAMGHRHKAGGÅGR 1174
                                                                                                                                                                                                                                                                                                                     UNLINAERVFSDNKDSKKQNLKNNSKDFND 1825
                                                                                                                                                                                                                                                                                                                                        QTAQTKREVPKNKAPTAEKRESGPKQAAV 1472
                                                                                                      KDLLDDSDDDDIEILEECIISAMPTKSSR 1589
                                                                                                                                                          QNRLQPQKHVSFTPGDDMPRVYCVEGTPI 1649
                                                                                                                                                                           SHKPFRVKKIMDQVQQASASSAPNKNQL 1765
                                                                                                                                                                                                                                                                                             1194
                                                                                                                        ATSGNGQGSTTR-----MDHETASVLSSS 295
              QG-----PPEATQFSLQWESYVKRFLD 967
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nin but its zygotic expression
Armadillo.";
7(1997).
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ycera; Muscomorpha;
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225 STRISAND TO THE TOTAL OF TH	925 SLDESGKANQAIVGTDADIKPKLEKQEEQE954	1338 QGSSLSSESARHKAVEPPSGAKSPSKSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFE 1397	1398 SRSIASSVQSEPCSGWVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQTAQTKREV 1452 1	1453 PKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTILHFATESTPDGFSCSSLSALSLD 1512 	1513 BPFIQKDVELRIMPPVQENDNGNETESEQPKESNENGEKE-AEKTID 1558	1559 SLDDDSDDDDI 1572	1573 -EILEECIISAMPTKSSRKGKKPAQTASKLPPPVARK-PSQLPVYKLLPSQNRLQPQKHV 1630	1631 SFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQSGEFEK 1686	1687 RDTIPTEGRSTDEAQGGKTSSVTIPELDDNKABEGDILAEC	1728INSAMPKGKSHKPPRVKKIMDQVQQASASSAPNKNQLDGKK 1769 	1770 KKPTSPVKPIPQNTEYRTRVRKNADSKNNLNAER 1803 	1804 VFSDNXDSK-KQNLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRND 1860	1861 SLSSLDFDDDDVDLSREKABLRKAKENKESEBAKVTSHTELTSNQQSANKTQA-IAKQPI- 1918 	1919 -NRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLONFAIENTPVCF 1963  :	1964	1996 QGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPKKKK 2052	2053 PSRLKGDNEKHSPRNMGGILGEDL/TLDLKDIQRPDSEHGLSPDSENFDWKAIQEGA 2108	2109 NSIVSSLHQAAAAGLSRQASSDSDSILSIKSGI-SLGSPFHLTP 2152       : :         :	2153 DQEEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQ 2212 :
ELEREMEBERSIDRAFBEGGRAQOQOLDELPPRNOGSSPASAGRESRSKEPSTILSRPLDOD  STISSAP  APPAPARLEMCANATTSPERGYTSSAVEATLGSKVECVYSILSRVGARDERAKKFLEL  SSODGCATLRRSGCMPLLYOWENDROVILGSKREAAAAAAAAHNVTSHPER  GSRAAGSCATLRRSGCMPLLYOWENDROWILGSKRAAAAAAAAHNVTSHPER  KASRREMTRAHLEQIDAYCSFLKTLAGSGGAIDDSBRHPL  SSODGCATLRRSGCMPLLYOWENDROWILGSKRAAAAAAAAAHNVTSHPER  KASRREMAKARLAGIUDYCSFLKTLAGSGGAIDDSBRHPL  SSODGCATLRRSGCMPLAYOWENDROWILGSKRAAAAAAANATNITTGOVA  SSODGCATLRRSGCMALAAAPHNTAGAKEDOWAGAAAAANATNITTGOVA  SSODGCATLRRSGCMALAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	ය 	& q	ò da	S S	<i>ે</i> ઇ વિ	g d	& a	<i>₹</i> 8	VQ dq	QV QD	% व	<i>₹</i> 8	\ <del>\</del> 43	λ d	승 유 -	& A	S qq	QY QD	Qy Dp
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                                                                                                                                                                                                                                                                                                                                                                                                            : | : | :: | :: | : | : : | 2304 GKSPAASRVVSGRVSSTIPPSRSNSNLNGSSAAAAAKINQAQSRIANIWKRVDEAKIK 2363
                                                                                                                                                                                                                                                                                                                                                                                                                                             PINS---TSQTVSSGATNGAESKTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGN 2678
                                                                                                                     -------OSP--GRNSISPGRNG----ISPPNKLS 2343
                                                                                                                                                                          2078 AMMQQFTFITDINIGHSQETCESTDHPEDAGESPECDQNSETESCDGQEPDHLPPPPSIV 2137
                                                                                                                                                                                                                                                SKGLNOMNNGNGANKKVELSRMSSTKS----SGSESDRSERPV-----LVRQSTF 2443
                                                                                                                                                                                                                                                                                                                                               2504 WRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVST 2563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2364 OSSSNIRTQKTKSSNMLNANGTKPTLLR----SSTFD------------------- 2397
                               1898 IKPPSIMDELLDSMISVDSIQSEVADGEQDCSMATTISVSNYETAACDDQTMTVLQSCFD 1957
                                                                                                                                                                                                   QL-----PRTSSPSTASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKNASSIPRSESA 2397
                                                                                                                                                                                                                                                                                               2444 IKEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGG 2503
                                                                                                                                                                                                                                                                                                                                                                                             WRRTGSSSSILSASSESSEXAKSEDEXHVNSISGTKOSKENOVSAK--GTWRKIKENEFS
                                                                                                                                                                                                                                                                                                                 -----KTPASKSPSEGQTATTSPRGAKPSVKSEL------SPVAR
                                                                                                       QTSQI-----GGSSKAPSRSGSRDSTPSRPAQQPLSRPI-------
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STRAIN-Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Nahburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Hell G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Rhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
          MKOP----LOANMPSISRGRIMIHIPGVRNSSSSTSPVSKKGPPL-
                                                                                                                                                                                                                         DERTSVVKPTTLEPATAVKLVRGRKKPAYVSPYSMQSQRN---
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Last annotation update)
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01-MAY-2000 (TEMBLEE) 13,
01-007-2003 (TEMBLEE) 25,
CG1451 protein.
APC OR CG1451.
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Borkova D., Botchan M.R., Bouck J., Broketein P., Brottier P.,

RA Cherry J.W., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.W., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.W., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dosler C., Gabriellan A.B., Gargen N.B., Galbart W.M., Glasser K.,

RA Fosler C., Gabriellan A.B., Gargen N.B., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Mei M.H., Ibegwam C.,

Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Lasko P., Lei Y., Levitsky A.A., Li J. J., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J. J., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J. J., J. Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Molland N.C., Molecod M.P., Mosherson D.,

RA Merulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Rainzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Rainzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Snith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Wang A.H., Wang X.,

Williams S.M., Woodage T., Worley R., Wang A.H., Wang S., Yao Q.A.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter E., Wang A.H., Wang S., Yao Q.A.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

R The genome sequence of Drosophila melanogaster.";

R Therby A. Probles P. Procentin binding, IDA.

R Therby T. Proposts. Readentin binding, IDA.

R Therby T. Proposts. Readentin binding, IDA. 337 248 SSSQDSCISMRQSGCLPLLIQLLHGNDKDSVLLGNSRGSKEARARASAALHNIHSQPDD 397 574 469 694 KRGRREIRVIHLIEQIRAYCETCWEWQEAHEPGM--DQDKNPMPAPVEHQICPAVCVLMK 455 | : | : | | : | : | : | : | ELREMREHRSLDRNFERQSAQQQQDLDELPPRNGGSPASAGRPSRSKEPSYTLSRFLDGD 635 GGGILRNVSSLIATNEDHRQILRENNCLQTLLQHLKSHSLTIVSNACGTLMNLSARNPKD 243 ERSSQNKHETGSHDAERQN-EGQGVGEINMATSGNGQGSTTR------MDHETASVLSSS 296 STHSAPR-----RLTSH-----LGTKVEMVYSLLSMLGTHDKDDMSRTLLAM 515 NKATLCSMKGCMRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLREVGSVKALME 575 CALEVKKESTLKSVLSALWNLSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIES LSFDEEHRHAMNELGGLQAIAELLQVDCEMYG-LINDHYSITLRRYAGMALTNLTFGDVA Gaps Query Match
12.1%; Score 1763; DB 5; Length 2417;
Best Local Similarity 25.3%; Pred. No. 3.4e-78;
Matches 720; Conservative 326; Mismatches 836; Indels 964; InterPro; IPR008938; ARM.
InterPro; IPR000225; Armadillo.
Pfan; PF00514; Armadillo\_seg; 5.
SMART; SM0108; ARM; 5.
PR05ETI; PS50176; ARM; EPPBAT; 2.
SEQUENCE 2417 AA; Z61282 MW; 08327727C475F254 CRC64; 129 338 249 398 456

Page 12

us-09-442-489f-2.rspt

933 -NTYNFTKSENSNRTCSMPYAKLEYKRSSNDSLNSVSSNDGYGKRGQMKPSIESYSEDDE 991 277 CRGPEGGRREAGSRAHPLARLKAAHASLSNDSLNSGSASDGYCPREHM	1172 HVDQPIDYSLKYATDIPSSGKQSFSFSKSSSGQSSKTEHMSSSEBNTSTPSSNAKRÇNQL 1231 383 HVPLLEGASRAGAEPLAGPGISPGARKGAWL 413 1232 HPSSAGSRGQPQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSAEDEIGCNQ 1291 414PADHLSKVPEKLAAAPL-SVASKALQKLAAQEGFLSLSRCSSLSSA-GRFGPSE 468 1292 TTQEADSANTLQTAETKGKTGTRSAELDPVSEVPAVSQHPRTKSSRLQGSSLSSESARHK 1350	469 GGDLDDSDSGLEGLEEAGPSEABLDSTWRAPGATSLP	GPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSLSALSLDEPFIQKDVEL	1643 CVEGTPINESTATSLEDITIESPPNELAAGEGVRGAQSGEFEKRITIPTEGRSTDEAGG 1702	1814 QNLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRNDSLSSLDFDDDDVD 1873   1814 QNLKNNSKDFNDKLPRNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRNDSLSSLDFDDDDVD 1873   1866 PG
8 4 6 6 6 6 6	8 8 8 8	4 6 6 6	6 6 6 6 6	8 8 8 8	8 8 8 8 8 8
QY 2489 PDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWK 2548    :     :     :     :     :	SUL		ED CUIT. BIOÎ. 9:105-108(1999).  DR EMBL, AJ31187; CAAA1317.1;  DR GO.0005578; C:extracellular matrix; IEA.  DR GO; GO:0004222; F:metalloendopetidase activity; IEA.  DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  DR InterPro; IPR000838; ARM.  DR InterPro; IPR001818; Pept_MIOA_MI2B.  DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.  FT NON TER.  SQUENCE 1685 AA; 175540 MW; B9B81923F3912F77 CRC64;	Query Match         11.7%;         Score 1705;         DB 4;         Length 1685;           Best Local Similarity 28.4%;         Pred. No. 1.5e-75;         Matches 636;         Gaps 85;           Matches 636;         Conservative 271;         Mismatches 672;         Indels 660;         Gaps 85;           QY         654 QILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQRALMDGAVSMLKNLIHS 713         Db         1 QVLRDHNCLQTLLQHLTSHSLTIVSNACGTLWNLSARSARDQELLWDLGAVGMLRNLVHS 60           QY         714 KHKMIAMGSAAALRNLWANRPAKYK-DANIMSPGSSLPSLHVRKOKALBAELDAQHLSET 772         QV	

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MEDINE=20196006; PubMed=10731132;

Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Galle R.F.,

R.A. Adams M.D., Celliker S.E., In P.W., Hoskins R.A., Galle R.F.,

R.A. Adams M.D., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

R. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

R. Sutton G.G., Mortman J.R., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

R.A. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

R.A. Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshkov S.,

Berkova D., Botchan M.R., Bouck J., Brokstein P., Bortcher P.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotcher P.,

R. Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

R. Borkova D., Botchan M.R., Dong Z., Mays A.D., Dew I., Dietz S.M.,

A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Bodson K., Doup D.E., Downes M., Dugan-Rocha S., Pleischmann W.,

R. Borts G. M., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

R.A. Glodek A., Gong F., Gerrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DECURINE 2235468; TISSUE Cerebellum; STRAIN=CSPEL/60; TISSUE=22354685; PubMed=12466851; The FAINTOM Consortium, The FAINTOM Consortium. The RAINTOM Consortium. The RINKEN Genome Exploration Research Group Phase I & II Team; Lanalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002). EMBL; AR080724; BAC38587.1; -. SEQUENCE 324 AA; 36909 FW; D74E29ECD952DICC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTDMTRRQLEYEARQIRAAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRVRQLLQSQAA
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Eukaryota, Metazoa, Arthropoda; Haxapoda; Insecta, Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Bphydroidea; Drosophilidae; Drosophila.
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EAERSSQSRHDAASHEAGRQHEGHGVAESNTAASSSGQ 276
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Pred. No. 5.3e-54;
9; Mismatches 14
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Best Local Similarity 91.0%;
Matches 253; Conservative
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APC2 OR E-APC OR CG6193.
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[1]
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                         PAVHPRGREPAVT-------KDPGPGGRDSSPSP---RAAEELLQRCISSALPRRRP 1024
                                                                                                                                                                                                                RAIQEGANSIVTWLHQAAAA---TREASSESDSILSFVSGLSVGSTLQPPKHRKGRQAEG 1125
                                                                                                                                                                                                                                                                                                     1126 EMGSARRÞ------EKRGAASVKTSGSPRSPAGPEK---------PRGTQKT 1162
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                                                                                    P-SRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRP---DSEHG----LSPDSENFDW
                                                                                                              KAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGS----PFHLTPDQEEK
                                                                                                                                                                                                                                                            PFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGOMKOPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIQSPGRNSISPGRNGISPPNKLSQLPRTSSPSTASTKSSGSGKMSYTSPGRQMSQQNLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2380 KQTGLSKNASSIPRSESASKGLNQMNNGNGA-NKKVELSRMSSTKSSGSESDRSERPVLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSKHSSSLPRVSTWRRTGSSSS1LSASSESSEKAKSEDEKHVNSISGTKQSKENQVSAKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2665 PINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNGSVPMRTVGLENRLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GSDVDGPSLAKAPIS----APFVHEGLGVAVGGFPASRHGSPSR--SARV
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Adenomatosis polyposis coli.
Mus musculus (Mouse)
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Hostin D., Houston K.A., Howland T.J., Wei MH., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketc Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin Lu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi P. Moulson B.M., Moly M., Murphy B., Murphy L., Muzny D.M., Nelson Nelson D.R., Palson Nelson R.A., Nixon K., Nusskern D.R., Parleb J., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rees	Reinert K., Remington K., Shue B.C., Siden-Kiamos I., Spier E., Spradling A.C., Svirskas R., Tector C., Tun Wang ZY., Wassarman D.A., Williams S.M., Woodage T.,	Ye J., Yeh RF., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zha Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Sm Gibbs R.A., Wyers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195 (2000).	00 M = 0 Z		DR EMBL; AE003746; AAFS6249.1; DR EMBL; AF013913; AAD40227.1; DR EMBL; AF013913; AAD40925.2; DR PRDS: AF091430; AAD20985.2; DR PLYBASE; FBGN00255598; ARM. DR InterPro; IPR008938; ARM. DR InterPro; IPR00125; Armadillo. DR PRAMT; SMO0185; ARM; 6. DR SWART; SMO0185; ARM; 6. DR SWART; SO10185; ARM REPEAT; 1. SQ SEQUENCE 1067 AA; I16702 MW; 20C8F5F6121888F8 CRC64;	Ouery Match Best Local Similarity 26.3%; Pred. No. 6.1e-52; Matches 429; Conservative 177; Mismatches 380; Indels 647; Gaps 50;  Oy 329 DWSRTLLAMSSSQDSCISMRQSGCLPLLIQLLHGNDXDSVLLGNSRGSKEARARASAALH 388  :::     :   :	OY 389 NITHSOPDDKRGRREIRVIHLLEDIRAYCETC-WEWQEAHEP-CMDQDKNPMPAPVEHQI 446  63 NIVHNNPEEKERQREYGRLLDQILDYCNFLHTQLQSGGEAIADDEDRHPL 114  QY 447 CPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQVDCEMYG-LTNDHYSITLRRYAGNAL 505  115 -AAMKLLAKASPDEEHRCTMCELGALKALPNHYHLDHYVHGPPAGREQCNALRSYGLAL 173	506 TNLTEGDVANKATLCSMKGCMRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTL   174 TNLTFCDENVHNKSYLCGGRQPHEVVIAQLNTAPDELLQVIAGVLRNLSWRADKHMKTIF 564 REVGSVKALMECALEVKKESTIKSVLSALMNLSAHCTENKADICAVDGALAFLVGTLTRR	294 GPSKTLKIIENAGGILRNVSSHIAVCEPYRQILRRYNCLAILLQQLKSESLTVVSNSCGT

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606;
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Adenomatosis polyposis coli tumor suppressor (Fragment)
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vative 0; Mismatches 0;
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Hum. Genet. 106:101-107(2000).
EMBL; AF127034; AAF34355.1; -.
InterPro; IPR008938; ARM.
InterPro; IPR000225; Armadillo.
PFam; PF00514; Armadillo.seg; 2.
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Su L.K., Steinbach G., Sawyer J.C.,
"Genomic rearrangements of the APC
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A traubberg R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,

A ltschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A ltschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Haieh F.,

A papleton M., Soares M.B., Moore T., Max S.I., Wang J., Haieh F.,

B piatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A papleton M., Soares M.B., Bonaldo M.F., Casvainci P., Prange C.,

B rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Rosak S.A., McEwan P.J., McKernan K.J., Mallek J.A., Gunarathe P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Rayminski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R Jones S.J., Marra M.A.,

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01-0CT-2003 (TrEMBLrel. 25, Created)
1-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primateg; Catarrhini; Hominidae; Homo.
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC056268; AAH56268.1; -
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US-09-442-489F-2 14575 1 MAAASYDQLLKQVEALKMEN......ESSGTQSPKRHSGSYLVTSV 2843 Title: Perfect score:

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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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geneseqp1980s:\*
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geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\*

## SUMMARIES

SUMM.  1D   AAR2605  AAR3539  AAR3530  AAR6350  AAR6310  AAR7210  AAR7278  AAR7278  AAR7278  AAR7278  AAR7278  AAR7278  AAR7278  AAR7278  AAR7278  AAR7278  AAR7278  AAR7278  AAR7370  AA	SUMMARIES	Description	2 Aar26052 APC gene	2 Aaw35392 Huma	0 Aaw38370 Human ade	4 Abg90964 Human ade	7	0 Aaw76140 Human	4 Human	1 Aab23011 Human	5 Abg71105 Human	Н	o.	4	4 Aar58634	AAR63508 Adenomato	Abg9096	AAW11922 Adenomato		AAB23012 Human APC		ABG71106 Auman ade	Human	4 Aab50674 Mouse APC	35 Abg09335 Novel hum	Human	Aaveolf1 Himan AbC
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26	27	28	53	30	31	32	33	34	35	36	37	38	ტ ტ	40	41	42	43	44	45

## ALIGNMENTS

neoplasm; cancer; oncogene; tumour; growth; detection; diagnosis; prognosis; treatment; sporadic colorectal carcinomas; ss. APC gene product in familial adenomatous polyposis. AAR26052 standard; protein; 2843 AA. (revised)
(first entry) 25-MAR-2003 28-JAN-1993 AAR26052; RESULT 1 AAR26052 

Homo sapiens.

WO9213103-A1. 06-AUG-1992.

(UYJO ) UNIV JOHNS HOPKINS. (ICIL) INPERIAL CHEM IND PLC. (UTAH ) UNIV UTAH. (CANC-) CANCER INST. 91GB-00000963. 91US-00741940. 92WO-US000376. 16-JAN-1992; .6-JAN-1991; 08-AUG-1991;

White RL; Markham AF; Thliveris A, Anand R, Hedge PJ, I Groden JL, Joslyn G, Vogelstein B, Carlson ML, Kinzler KW, Albertsen H, Nakamura Y;

WPI; 1992-284685/34. N-PSDB; AAQ27234.

Detection of somatic and germ-line alterations of human APC gene - used to diagnose, treat and study familial adenomatosus polyposis and sporadic colorectal cancer.

Disclosure; Page 47; 132pp; English.

This sequence is encoded by the APC (Adenomatous Polyposis Coli) generassociated with tumorigenesis, found on chromosome Sq. The sequence may be mutated by deletions insertions, investions, or point mutations of the gene. The APC gene is expressed in most normal tissues as well suggesting that APC is a tumour suppressor. (Updated on 25-MAR-2003 to correct PN

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	### SCHPRTKSSRLQGSSLSSESARHKAVEFPSGAKSF ####################################	Db 1961 SISSLDFDDDDVDLSREKAEIRKAKENKESEAKVTSHTELTSNQGSANKTQAIAKQPINR 1920  Qy 1921 GQPKPILQKOSTFPGSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSDDDDGENN 1980  Db 1921 GQPKPILQKOSTFPGSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSDDDGENN 1980  Qy 1981 NKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQ 2040  Db 1981 NKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQ 2040  Qy 2041 BCISSAMPKKKPSRLKGDNBKHSPRNMGGILGEDLTLDLKOIQRPDSEHGLSPDSENFD 2100
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field.) (Updated on 25-MAR-2003 to correct PI field.)  Sequence 2843 AA;  Query Match  Best Local Similarity 100.0%; Pred. No. 0;  Matches 2843; Conservative 0; Mismatches 0; Indels 0; Gaps 0;    MAAASYDQLLKQVEALKAENSNLRGELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM 60	BABEASSONKHETCSHDABERQUEGGGGGGGGGGTTRNDHETASVLSSSSTHSA BABEASSONKHETCSHDABERQUEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	781 PKASHKSKQARKOSLYGDYVEPDINKHDDNRSDNFNITANITANITANITANISSSSSKOS 840 781 PKASHRSKQARKQSLYGDYVEPDINRHDDNRSDNFNITGNITALSPYLNITYLPSSSSSSKOS 840 781 LDSSRSEKDRSLERERGIGLGNYHPATENPOTISSKRCLQISTTAAQIAKVMEEVSAIHTS 900 841 LDSSRSEKDRSLERERGIGLGNYHPATENPOTISSKRCLQISTTAAQIAKVMEEVSAIHTS 900 841 LDSSRSEKDRSLERERGIGLGNYHPATENPOTISSKRCLQISTTAAQIAKVMEEVSAIHTS 900 901 QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS 960 901 QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS 960 901 QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS 960 901 QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS 960

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The present sequence is the human adenomatous Polyposis coli (APC) gene product, which was used in the development of a novel method of diagnosing or prognosing an APC gene associated neoplastic tissue. The method comprises comparing APC gene coding sequences or mRNA in a tumour tissue, to APC gene coding sequences or mRNA in a non-neoplastic tissue, tumour tissue. APC is a tumour repressor expressed in most normal tissues. APC mutations are found in familial adenomatous polyposis and sporadic colorectal cancer patients. The method enables mutations to be detected to provide an indication of predisposition to cancer. (Updated on 25-MAR-2003 to correct PR field.)
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Groden J, Carlson M, Kinzler K; Vogelstein B, Thliveris A, Anand R,

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61 ASSGQIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR
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Human; adenomatous Polyposis coli; APC; diagnosis; prognosis; neoplastic tissue; tumour tissue; tumour repressor; mutation; sporadic colorectal cancer; detection.

Homo sapiens

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Human adenomatous Polyposis coli gene product.

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tissues. APC mutations are found in familial adenomatous polyposis and sporadic colorectal cancer patients. The method enables mutations to be detected to provide an indication of predisposition to cancer. (Updated on 25-MAR-2003 to correct PK field.)
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Hedge PJ, Carlson M, Anand R, Thliveris A, Albertsen H, White
Joslyn G;
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16-JAN-1991;
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                                                                                      1 MAAASYDQLLKQVBALKMENSNLRQELEDNSNHLTYKLETEASNMKEVLKQLQGSIEDEAM
                                                                                                                                   61 ASSGQIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR
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                                                                 1 MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM
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100.0%; Score 14575;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2843; Conservative 0; Mismatches
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Hedge PJ, Joslyn s A, Vogelstein B; Groden J, Hedg , Thliveris A, Carlson M, G JAPANESE FOUND CANCER RES 91GB-0000962. 91GB-0000963. 91GB-0000974. 91GB-0000975. 91US-00741940. 95US-00449731 JOHNS HOPKINS. UTAH. Anand R, Markham AF, WPI; 2002-641559/69. N-PSDB; ABS67119. ZENECA LTD Albertsen H, Kinzler K, Ma White RL; 16-JAN-1991; 16-JAN-1991; 16-JAN-1991; 08-AUG-1991; 12-AUG-1994; VIND US6413727-B1 25-MAY-1995; 02-JUL-2002 (UYJO) (UTAH) (NICA-) (ZENE) 

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Method to aid in the diagnosis/prognosis of neoplastic tissues in humans, by detecting somatic alteration of wild-type APC protein in tumor tissue isolated from human, the alteration indicating neoplasia of the tissue.

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Disclosure, Fig 3, 140pp, English

This invention relates to a novel method to aid in the diagnosis or prognosis of a neoplastic tissue of a human. The method involves detecting somatic alteration of wild-type adenomatous polyposis coli) protein in a tumour tissue isolated from a human (the alteration indicating neoplasia of the tissue). The method of the invention is method is useful in diagnosis or prognosis of a neoplastic tissue of a human. the method is useful in detection of genetic predisposition to cancer. The present sequence represents a protein sequence used in the method of the invention

Sequence 2843 AA

EAERSSONKHETGSHDAERQNEGGGVGEINMATSGNGGGSTTRWDHETASVLSSSSTHSA 300 d ö 240 240 PRRLISHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMROSGCLPLLIQLL 360 420 120 120 180 180 EAERSSQNKHETGSHDAERQNEGQGVGEINMATSGNGQGSTTRMDHETASVLSSSSTHSA 300 PRRITSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLLAMSSSQDSCISMRQSGCLPLLIQLL 360 09 9 QTDLTRRQLEYBARQIRVAMBEQLGTCQDMBKRAQRRIARIQQIEKDILRIRQLLQSQAT ASSGQIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR RGFVNGSRESTGYLBELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL QTDLTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT MAAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM MAAASYDQLLKQVBALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQVGSSIEDEAM ASSGOIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR HGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDDKRGRREIRVLHLLEQIRAYCETC Gaps ö Length 0; Indels 5; g Score 14575; ; Pred. No. 0; 0; Mismatches 100.0%; Best Local Similarity Matches 2843; Conservative 61 61 121 121 181 181 241 241 301 301 361 Query Match 8 6 8 8 \$ 6 \$ 6 6 \$ 6 \$ 음 상

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1080 1020 480 480 540 540 009 900 999 999 720 720 780 780 840 840 900 900 096 096 GSAAALRNI,MANRPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLS SSGOSSKTEHMSSSSENTSTPSSNAKRQNQLHPSSAQSRSGQPQKAATCKVSSINQETIQ TYCVEDTPICFSRCSSLSSAEDEIGCNOTTORADSANTLOIAEIKGKIGTRSAEDPV PPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGF HGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDDKRGRREIRVLHLLEQIRAYCETC 421 WEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQ UDCEMYGLTNDHYSITLRRYAGMALTNLFGDVANKATLCSMKGCMRALVAQLKSESEDL ENKADI CAVDGALAFLVGTLTYRSQTNTLAI I ESGGGILRNVSSLIATNEDHRQILRENN CLOTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSKHKMIAM CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQBALWDMGAVSMLKNLIHSKHKMIAM GSAAALRNIMANRPAKYKDANIMSPGSSLPSIHVRKOKALEAELDAQHLSETFDNIDNLS PKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSRGS QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS NDSLNSVSSNDGYGKRGOMKPSIESYSEDDESKFCSYGOYPADLAHKIHSANHMDDNDGE NDSLNSVSSNDGYGKRGOMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGE LDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHIIEDEIKQSEQRQSRNQSTTYPVYTE LDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHIIEDEIKQSEQRQSRNQSTTYPVYTE STDDKHLKFQPHFGQQECVSPYRSRGANGSTNRVGSNHGINQNVSQSLCQEDDYEDDKP TNYSERYSEEEQHEEEERPTNYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSKS SSGQSSKTEHMSSSSENTSTPSSNAKRQNQLHPSSAQSRSGQPQKAATCKVSSINQETIQ SEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFPSGAKSPSKSGAQTPKSPPEHYVQET PLMFSRCTSVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPP PLMFSRCTSVSSLDSFESRSIASSVQSEPCSGWVSGIISPSDLPDSPGQTMPPSRSKTPP WEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQ VDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCSMKGCMRALVAQLKSESEDL ENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRENN PKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSRGS LDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTS LDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTS STDDKHLKFQPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKP TNYSERYSEEEQHEEEERPTNYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSKS QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS TYCVEDTPICESRCSSLSSAEDEIGCNOTTQEADSANTLQIAEIKGKIGTRSAEDPV SEVPAVSOHPRTKSSRLOGSSLSSESARHKAVEFPSGAKSPSKSGAQTPKSPPEHYVQET 901 196 196 1021 1021 1081 1141 1141 1201 1201 1261 1261 1321 1321 1381 1381 1441 481 601 661 721 781 781 841 841 1081 361 481 601 661 721 901

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                                                                                                                                                                                                                                                                                     PFSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVNNNTKKRDSKT
                                                                                                                    KTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDN
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                SEKAKSEDEKHVNSISGTKOSKENQVSAKGTWRKIKENEFSPINSTSQTVSSGATNGAES
                                            2581 SEXAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFSPTNSTSQTVSSGATNGAES
                                                                                           KTLIYQMAPAVSKTEDVWYRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDN
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Joslyn G;
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                                                                                                                                                                                                                                                                                                        SGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKP 1740
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                                        SCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSE
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cancers such as familial adenomatous polyposis (FAP) and Gardner's syndrome. The wild type APC gene (or a part of it) can be used the respontant of the restore gene function, while primers and probes detect mutations. Also APC proteins or analogues can be used to detect mutations. Also APC proteins or analogues can be administered to compensate for a defective gene, and epithelial cells, or transgenic animals carrying a mutated APC allele are useful for detecting corrior agents able to suppress tumorigenesis. (Updated on 25-MAR-XX Secuence 2860 AA;

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therapeutic agents able to suppress tumorigenesis. (Updated on 25-MAR- 2003 to correct PA field.) Sequence 2860 AA;	ery Match 99.8%; Score 14551; DB 2; Length 2860; st Local Similarity 99.4%; Pred. No. 0; tches 2842; Conservative 0; Mismatches 0; Indels 18; Gaps	2 AAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAMA	62 SSGQIDLLERLKELNLDSSONFOGVKLRSKØSLRSYGSREGSV	61 SSGQIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSNFPGVKLRSKMSLRSYGSREGSV	104 SSRSGECSPVPMGSFPRRGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDMYYAQLO	64 NLTKR	181 NLTKRIDSLPLTENFSLQTDLTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQ	(1)	- 14. - 1	284 MDHETASVLSSSSTHEAPRRITSHLGTKVEMYSLLSMLGTHDKDDMSRTLLAMSSSQUS		344 CISWRQSGCLPLLIQLLHGNDKDSYLLGNBRGSKRARARARASAALHNIIHSQPDDKRGRRR 	04 I	421 IRVLHLIBQIRAYCETCWEWQEAHEPGMDQDKNPNBAPVEHQICPAVCVIMKLSFDEEHR	464 HAMNELGGLQAIAELLQVDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCSNK	481 HAMNELGGLQAIAELLQVDCEMYGLINDHYSITLRRYAGMALTNITFGDVANKATLCSMX	524 GCWRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKES	84 TLKSVLSALWNLSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIE	601 TLKSVLSALWNLSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVS	41 '	61 8	704 VSMLKNLTHSKHKMTAMGSAAALRNLMANRPAKYKDANIMSPGSSLPSLHVRKQKALEAE	721 VSMLKNLIHSKHKMIAMGSAAALRNLMANRPAKYKDANIMSPGSSLPSLHVRKQKALEAE	764 IDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLS	781 LDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYVFDINRHDDNRSDNFNTGNMTVLS	824 PYLNITVLPSSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTT
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≿ &	901	AAQIAKVMEEVSAIHTSQEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFYKSENS 943 
	944	NRTCSMPYAKLEYKRSSNDSLNSVSSNDGYGKRGQMKPSIESYSEDDESKFCSYGQYPAD 1003
£ 6	1004	LAHKIHSANHMDNDGELDTPINYSLKYSDBOLNSGRQSPSONERWARPKHIIEDBIKQS 1063
<i>ই</i> ;	90	40STTYPVYTESTDDXHLKFQPHFG
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٠ کې ځ	1244	QKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSAEDEIGCNQTTQEADSANTLQ 1303
à	30	KGKIGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFPSGAKSPS
op q	1321	—д
oy G	1364	SGAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFESRSIASSVQSEPCSGVVSGIISPSDL 1423 
λά	1424	DSPGCIMPPSRSKIPPPPPQIAQIKKEVPKNKAPTABKRESGPKQAAVNAAVQRVQVLP 148
qq	1441	SPGQTMPPSRSKTPPPPPQTAQTKRBVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLP 150
٠ کې ځ	1484	DADTLIHPATESTPDGFSCSSSLSALSLDEPPIQKDVELRIMPPVQENDNGNETESRQPK 1543  [
3 &	54	SNENQEKEAEKTIDSEKOLLDDSDDDIEILEECIISAMPIKSSKKKKKRAQTASKLPP 160
o QQ	1561	SNENQEKEAEKTIDSEKDLLDDSDDD1E1LEECI1SAMPTKSSRKGKKPAQT
à à	1604	PVARKPSQLPVYKLLPSQNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIE 1663
3 8	vi vi	VANATSAGLI VIIGILI SANASSA KANDI PITEGRSTDEAQGGKTSSVII PELDDNKAEEGDI 172
연	9	SPPNELAAGEGVRGGAQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGD
οχ	1724	LAECINSAMPKGKSHKPPRVKKIMDQVQQASASSAPNKNQLDGKKKKPTSPVKPIPQNT 1783
qq	1741	LAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSAPNKNQLDGKKKKPTSPVKPI
ò	7	EVRITRVRKNADSKANLANAERVFSDNKDSKKQNLKANNSKDFNDKLPNNEDRVRGSFAFDSP 184
qq	1801	EYRTRVRKNADSKNNLNAERVFSDNKDSKKQNLKNNSKDFNDKLPNNEDRVRGSFAFDSF 186
& A	1844	HHYTPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSN 1903
ζ		QOSANKTQAIAKQPINRG

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This sequence represents a human familial adenomatous polyposis colinkable) protein from clone DP2.5. The gene for the protein is present on human chromosome 521 and is also referred to as adenomatous polyposis coli gene. It is a tumour suppressor gene, and mutations in this gene tumours, and especially familial adenomatous polyposis (FAP) and despecially familial adenomatous polyposis (FAP) and colorectal tumours, and especially familial adenomatous polyposis (FAP) and calculated with tumourigenesis in retinoblastoma and colorectal tumours, syndrome (GS). The protein can be used in therapy to replace lack of native functional protein and the nucleic acids can be used for gene therapy. The nucleic acids that encode them can also be used as probes and primers in detection of the cancers and predisposition to it. (Updated on 25-MAR-2003 to correct PR field.)
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                  Familial adenomatous polyposis coli, APC, tumour suppressor, therapy, chromosome 5q21; tumourigenesis, retinoblastoma, colorectal tumour, FAP; Gardner's Syndrome, GS; predisposition.
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Albertsen H;
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Nakamura Y,
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Best Local Similarity 99.8%;
Matches 2836; Conservative
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Thliveris A, Groden J,
Vogelstein B, Hedge ÞJ;
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N-PSDB; AAV56447.
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                                                                                                        NSSLSSLSIDSEDDLLQECISSAMPKKKKPSRLKGDNEXHSPRNMGGILGEDLTLDLKDI
                                                                                                                           QRPDSEHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGIS
                                                                                                                                                                                                                                                                                                                      RSNSEISGOMKOPLOANMPSISRGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSE
                                                                                                                                                                                                                                                                                                                                                  RSNSEISGQMKQPLQANMPGISRGRTMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSE
                                                                                                                                                                                                                                                                                                                                                                                          GQTATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2461 IKEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGG
                                  SHNSSLSSLSDIDQENNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSR
                                                                                                                                                                                                                                                LGSPFHLTPDQEEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGRNS I SPGRNG I SPPNKLSQLPRTSSPSTASTKSSGSGKMSYTSPGRQMSQQNLTKQTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2504 WRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2641 NSTSQTVSSGATNGAESKTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSVSEKANPNIKDSKDNQAKQNVGNGSVPMRTVGLENRLISFIQVDAPDQKGTEIKPGQN
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241 EAERSSQNKHETGSHDAERQNEGQGVGEINMATSGNGQGSTTRNDHETASVLSSSSTHSA 300

QTDWTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDIIRIRQLLQSQAT

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(first entry) (revised)

25-MAR-2003 23-NOV-1998

BXHHXXX

RESULT 6 AAW76140 Human APC protein #1.

	241	. EAERSSQNKHETGSHDAERQNEGQGVGEINMATSGNGQGSTTRMDHETASVLSSSSTHSA 300		
	301	PRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLLAMSSSQDSCISMR	à	81 PLMFSR
	301	PRILISHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL 360	q <sub>Q</sub>	1381 PLMFSRC
	361	HGNDKDSVLLGNSRGSKEARASAALHNIIHSOPDDKRGRREIRVIHLLEOIRAYCETC 4	ò	1441 PPPQTAQ
	361		qq	- 14
	421	WEWOEAHERGYNDODKNPMPAPVEHOICPAVCVIMKISPDEEHBHAMNEIGGIOAIAEIIO 48	ò	1501 SCSSSLS
	421		q <sub>C</sub>	~ທ
	481	VDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCSWKGCMRALVAOLKSESEDL 5	λŏ	1561 KDLLDDS
	481	VDCEMYGLINDHYSITLRRYAGWALTNLFFGDVANKATLCSMKGCMRALVAQLKSESEDL	qQ	1561 KDLLDDS
	541	QQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWNLSAHCT	ζō	1621 QNRLQPQ
	541	QOVIASVIRNLSWRADVNSKKTIREVGSVKALMECALEVKKESTIKSVISALMNLSAHÇT	qq	_
	601	ENKADI	ò	1681 SGEFEKR
	601	BNKADICAVDGALAFLVGTLITYRSQTNTLAIIESGGGILRNVSSLIAINEDHRQILRENN	qi -	
	661	CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQBALWDWGAVSMLKNLIHSKHKMIAM 720	& E	1741 FRVKKIM         1741 FRVKKIM
	661	CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLHS	3 8	
	721	GSAAALRNIMANRPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLS 78	γ d	1801 AERVESD
	/21	GSAAALKNLMANKPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLS 78	ò	1861 SLSSLDF
	781	PKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLFSSSSSRGS	qq	1861 SLSSLDF
	2 6	I.DSSRRKTNRGI RPERIOTICALANYHAMINDORASAKATI AMITA METALAMIN METASOSOSOKO OT	ò	1921 GQPKPIL
	841	LDSSRSEKORSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTS	a a	1921 GQPKPII
	901	OEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS	λõ	1981 NKENEPI
	901	QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS 9	qq	-2
	961	NDSLNSVSSNDGYGKRGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGE 1	ò	2041 ECISSAM
	961	NDSLNSVSSSDGYGKRGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDG	ପ୍ର	
	1021		ð 1	2101 WKAIQEG
	1021	. DTPINYSLKYSDEQLNSGRQSPSQNERWARPKHIIEDEIKQSBQRQSRNQSTTYPVYTE 1080	a :	
	1081	STDDXHLKRQPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDXEDDKP 114	<b>₹</b> 43	2161 SNKGPRI
	1081	STDDKHLKRPRHRGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKP	⋩	2221 MPSISRG
	1141	TNYGEKYGEEGGHEEEEKFINYSIKANEEKKHYDQPIDYGEKYAILFYSGOXGEFSKKX 1200 TNYGERYGERDHEEERPINYSIKANEKKHYDDPIDYSKYYDDIDSGOKOSGOSKK 1200	qq	111111 2221 MPSISRG
	1201	SSCOSSWITCHMSSSSENTED 1950 THE PROPERTY OF THE	λō	2281 ELSPVAR
	1201	SSGQSSKTEHMSSSSENTSTPSSNAKRONQLHPSSAGSRSGQPQKAATCKVSSINQET1Q 126		
	1261	TYCVEDTPICFSRCSSLS	<u> </u>	2341 KLSOLPR         2341 KLSOLPR
	1261	- [		
	1321	SEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEPPSGAKSPSKSGAQTPKSPPEHYVQET 13:	qq	   1
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2340 2040 2100 2100 2340 2460 2460 1440 1440 1500 1560 1620 1620 1680 1740 1800 1800 1860 1860 1920 1980 2040 2160 2160 2220 2220 2280 2280 2400 1560 1680 1920 1980 CTSVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGGTMPPSRSKTPP RDIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKP ILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQPLQAN SALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSE OKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAO QKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ RDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKP MDQVQQASASSSAPNKNQLDGKKKKPTSPVKPIPONTEYRTRVRKNADSKNNLN MDQVQQASASSSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLN FDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQPINR MPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD GANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPFT ILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQPLQAN GRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGQTATTSPRGAKPSVKS **OTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGF** QTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLIHFATESTPDGF SDDDDIEILEECIISAMPTKSSRKGKKPAQTASKLPPPVARKPSQLPVYKLLPS SDDDDIEILEECIISAMPTKSSRKAKKPAQTASKLPPPVARKPSQLPVYKLLPS FDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQPINR LOKOSTFPOSSKDIPDRGAATDEKLONFAIENTPVCFSHNSSLSSLSDIDQENN LOKOSTFPOSSKDIPDRGAATDEKLONFAIENTPVCFSHNSSLSSLDDQENN IKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQ MPKKKKPSRLKGDNEKHSPRNMGG1LGEDLTLDLKDIQRPDSEHGLSPDSENFD GRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGQTATTSPRGAKPSVKS ROTSOIGGSSKAPSRSGRDSTPSRPAQOPLSRPIQSPGRNSISPGRNGISPPN RISSPSTASTKSSGSGRMSYTSPGROMSQONLTKQTGLSKNASSIPRSESASKG

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This sequence represents a human familial adenomatous polyposis coli (APC) protein isolated from 87 cDNA clones. The gene for the protein is present on human chromsome 5021 and is also referred to as adenomatous polyposis coli gene. It is a tumour suppressor gene, and mutations in this gene have been associated with tumourigenesis in retinoblastoma and colorectal tumours, and especially familial adenomatous polyposis (PAP) and Gardner's Syndrome (GS). The protein can be used in therapy to replace lack of native functional protein and the nucleic acids can be used for gene therapy. The nucleic acids that encode them can also be used as probes and primers in detection of the cancers and predisposition to it. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTDLTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRRLISHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLIQLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.7%; Score 14533; DB 2; Length 2843;
llarity 99.8%; Pred. No. 0;
Conservative 2; Mismatches 5; Indels 0;
                    Disclosure; Col 63-78; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 2836; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2843 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adenomatous polyposis coli protein - useful in the treatment of cancers associated with mutation(s) on human chromosome 5q21.
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Nakamura Y,
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) UNIV JOHNS HOPKINS.
) UNIV UTAH.
) ZENECA PHARM.
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A. Groden J, A
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Thliveris A, G
Vogelstein B, I
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16-JAN-1991;
16-JAN-1991;
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The invention relates to a novel method for detecting Adenomatous

Polyposis Coli (APC) protein in a sample. The method involves contacting

the sample with antibodies which specifically binds to the 2813 amino

acid form of the human APC protein, or to a mutent APC protein, and

detecting an APC-antibody complex. Mutations in the APC gene play a role

in tumorigenesis, indicating that it is a tumour suppressor gene. It is

coated on chromosome 521, which corresponds to the FAP (familial

adenomatous polyposis) locus. FAP is an autosomal dominant inherited

disease in which affected individuals develop hundreds to thousands of

adenomatous polyposis in the colon and rectum, some of which progress to

malignancy. The FAP locus is often found to be deleted in sporadic (i.e.,

non-familia) adenomas and carcinomas, and chromosome 5q deletions have

also been observed in tumours of the lung, breast, colon, rectum,

con-familia) adenomas and carcinomas, and chromosome 5q deletions have

also been observed in tumours of the lung, breast, colon, rectum,

bladder, liver, sarroomas, stomach, and prostate, and in leukaemisas and

lymphomas. Although the FAP locus several other genes such as

FER, TBI, TB2, and MCC, it is thought that mutations in the APC gene play

a key role in the development of FAP and sporadic tumours. The method is

useful for detecting APC protein and its mutant forms in foeral tissue,

placental tissue amniotic fluid, blood, serum or a tumour sample. The

somatic alteration of wild-type APC genes, and for testing therapeutic

agents for the ability to suppress tumours. The present sequence

represents a 2843 amino acid splice variant of the human APC protein.

This variant is more abundant than the 2742 amino acid variant (ABB23012)
                                                                            APC gene; Adenomatous Polyposis Coli gene; human; chromosome 5q21; familial adenomatous polyposis; FAP locus; Gardner's syndrome; GS; sporadic tumour; adenoma; carcinoma; cancer; lung; breast; colon; rectum; bladder; liver; sarcoma; stomach; prostate; leukaemia; lymphoma; tumour suppressor; anti-APC antibody; detection; diagnosis; prognosis; genetic predisposition; drug screening; DP2.5; splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting Adenomatous Polypopsis Coli (APC) protein in a sample for diagnosing cancers, involves contacting the sample with antibodies t specifically bind to APC protein and detecting the complex formed.
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                                          Human APC protein (splice variant 1).
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91GB-00000963.
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, Thliveris A, Nakamura Y, Vogelstein B;
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2161 SINKEPRILIKPGERKSTLETTKIESESKGINGGRKKYVKRIJITGKVESNSEISGOWNOPLOAM 2220	EP1243646-A 25-SEP-2002 07-MAR-2002 19-MAR-2001
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                                                                                                                                                      The invention describes a transgenic Drosophila whose genome comprises allowing regulated human colon cancer gene Adenomatous Polyposis Coli (APC) allowing regulated mis-expression of the APC gene resulting in developmental abnormalities. The transgenic files are used to screen and validate efficacy of anticancer drugs, to identify new target proceins interacting with beta-catenin, genes which interact with human APC, to study the biochemical function of human APC and to identify additional components of the Drosophila Wat/Wg signalling pathway. In particular the files are used to screen potential drugs against colon cancer. This is the amino acid sequence of the human adenomatous polyposis coli (APC) protein DNA encoding which is incorporated in the transgenic flies
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                                                                                 New transgenic Drosophila containing the human colon cancer gene Adenomatous Polyposis Coli is useful as an assay model to screen for new drugs, particularly against colon cancer.
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Tcf; beta-catenin; human; drug; familial adenomatous polyposis; cancer; adenomatous polyposis coli; APC; neoplastic.
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Vogelstein B;
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           DSTESSGTOSPKRHSGSYLVTSV
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Morin PJ,

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This sequence represents a human APC protein which is used in a method of identifying candidate drugs for use in familial adenomatous polyposis (TAPP) patients, or patients with increased risk of developing cancer. The protein can also be used to determine the presence or absence in a cell of wild type adenomatous polyposis coli (APC) gene or a downstream or protein in the APC transcription regulatory pathway. This method involves introducing a TCF-responsive reporter gene into the cell, and measuring transcription of the reporter gene where a cell which supports active downstream protein of the APC transcription regulatory pathway. The protein can also be used in a method of diagnosing cancer in a sample cancer not other cancer associated with FAP, comprising administering to the patient a polypeptide comprising a patient with colorectal comprising the beta-catenin binding site
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Intron-free DNA encoding Tcf-4 protein - useful for, e.g. identifying drugs for treating FAP patients, or patients with increased risk of
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                    KLSQLPRTSSPSTASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKNASSIPRSESASKG
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The present sequence is a transcriptional activation protein related to the invention. The invention relates to human Tcf-4 proteins and their corresponding cDNA molecules which encodes transcriptional activation factorization consistency to be a catenin and cativates transcription in colorectal epithelial cells. Moreover it has been found that adenomatous polyposis coli (APC) regulates this consistency are recombinant adenovirus, Ad-Mini-Me ie., APC Minus its amino- and carboxyl -terminal Ends which expresses a fusion protein, consistency fluorescent protein (GFP)/CAPC containing GFP fused to the central control apoptosis or treating colorectal cancer. These fusion proteins inducing apoptosis or treating colorectal cancer, and other cancers care useful for treating cancer, e.g. colorectal cancer, and other cancers associated with Familial Adenomatous Polyposis (FAP) or patients with increased risk of developing cancer. Human Tcf-4 cDNA provides an excellent system for screening agents for their ability to promote callivery, integration, hybridization, expression, replication or integration in cells or in an animal. It also provides methods for diagnosis cancer in a sample suspected of being neoplastic
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99.8%; Pred. No. 0;
cive 2; Mismatches
Disclosure; Page 74-81; 83pp; English.
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Best Local Similarity 99.8
Matches 2836; Conservative
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DSTESSGTQSPKRHSGSYLVTSV 2843

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The present sequence is a protein involved in cancer diagnosis associated with APC or beta-catenin mutations. Human Tcf-4B protein expressed in colorectal epithalium transactivates transcription when associated with beta-catenin. Adenomatous polyposis coli (APC) regulates this transcriptional activation, at least in part by binding to beta-catenin. Determining wild-type APC protein for diagnosing cancer comprises introducing a Tcf responsive reporter gene having upstream sequences of MYC into a cell and measuring transcription of the reporter gene. The candidate drug identified is useful for treating familial adenomatous polyposis patients with APC or beta-catenin mutations and patients with increased risk of developing cancers such as colorectal, thyroid, brain, medulloblastoma, desmoid tumour, osteoma, breast, head and neck
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                                                                                                                                                                                                    Human Tcf-4B protein; transcription factor; beta-catenin;
Adenomatous polyposis coli; APC; transcriptional activation;
Tcf responsive reporter gene, APC transcription regulatory pathway;
familial adenomatous polyposis; PAP; cancer; colorectal; thyroid; brain;
medulloblastoma; breast; head; neck; desmoid tumour; osteoma; cytostatic.
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Pred. No. 0;
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protein; 2973
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Best Local Similarity 99.7
Matches 2835, Conservative
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AAY70304 standard;
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QTDLTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT 240

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ct germ line or somatic mutations indicating a cancer and possibly gastric, oesophageal, lung cancers. (Updated on 25-MAR-2003 to correct	Score 14521; DB 2; Length 2843; Pred. No. 0; 6; Mismatches 4; Indels 0; Gaps 0;	maaasydollkovbalkmensnlroelednsnhlykleteasnmkevlkologsiedeam 60 	SSGQIDLLERLKELNIDSSNPPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPWGSFPR 120 	RGFVNGSRESTGYLEELEKERSLILADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL 180 	OTDLTRROLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIROLLOSOAT 240 	EAERSSONKHETGSHDAERONEGGGVGEINMATSGNGGGSTTRMDHETASVLSSSŠTHSA 300 	PRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL 360 	HGNDXDSVILGNSRGSKEARARAALHNIIHSQPDDKRGRREIRVLHLLEQIRAYCETC 420 	WEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQ 480 	VDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCSMKGCMRALVAQLKSESBDL 540 	QOVIASVLENLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALMNLSAHCT 600 	ENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRENN 660 	CLOTILOHLKSHSLTIVSNACGTLWNLSARNPKDOBALWDMGAVSMLKNLIHSKHKWIAM 720 	GSAAALRNIMANRPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLS 780 	SKORHKOSLYGDYVFDINRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSRGS 840 	SRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTS 900	QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNITYNFTKSENSNRTCSMPYAKLEYKRSS 960
cancer. The Abs can detect g predisposition to colon cand pancreatic or small cell lun PN field.) Sequence 2843 AA;	99 6%; set Local Similarity 99.6%; tches 2833; Conservative	1 MAAASYDQLLKQVEALKWE 	61 ASSGQIDLLERLKELNLDS 	121 RGFVNGSRESTGYLBELER 	181 QTDLTRRQLEYEARQIRVA	241 EAERSSONKHETGSHDAEI            241 EAERSSONKHETGSHDAEI	301 PRRLISHLGTKVEMVYSLI             301 PRRLISHLGTKVEMVYSLI	361 HGNDKDSVLLGNSRGSKE.                361 HGNDKDSVLLGNSRGSKE.	421 WEWGEAHEPGMDODKNPM	481 VDCEMYGLTNDHYSITLE:	541 QOVIASVLRNLSWRADVN 	601 ENKADICAVDGALAFLVG	661 CLQTLLQHLKSHSLTIVS	721 GSAAALRNIMANRPAKYK                721 GSAAALRNIMANRPAKYK	781 PKASHRSKQRHKQSLYGDYV 	841 LDSSKSEKDRSLERERGI 	901 QEDRSSGSTTELHCVTDE
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            SNKGPRIIKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQPLQAN
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                                              WKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPFT
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New human adenomatous polyposis coli DNA encoding tumour repressor - derived primers and probes for diagnosis, prognosis and treatment of

cancer.

Kinzler

Anand R, Nakamura Y, Groden J, Kinzle: , Vogelstein B, Albertsen H, White RL;

Markham AF, Hedge PJ, A Thliveris A, Carlson M, Joslyn G;

WPI; 1994-316233/39. N-PSDB; AAQ72297.

91GB-00000962. 91GB-00000963. 91GB-00000974.

16-JAN-1991; 16-JAN-1991; 16-JAN-1991;

(ICIL ) IMPERIAL CHEM IND. (CANC-) CANCER INST. (UYJO ) UNIV JOHNS HOPKINS. (UTAH ) UNIV UTAH.

91US-00741940

08-AUG-1991; 16-JAN-1991;

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AAC72297 is a cDNA isolated from the human adenomatous polyposis coli AAR63507 and AAR63509. Determination of alterations in APC or its expression products, can be used for the diagnosis and prognosis of cancer e.g. colorectal, lung and breast tumours; and for determining predisposistion to certain cancers such as familial adenomatous polyposis (PAP) and Gazdner's syndrome. The wild type APC gene (or a part of it) can be used the therapeutically to restore gene function, while primers and probes derived from the cDNA (AAQ72813-400 and AAQ72811-568) can be used to detect mutations. Also APC proteins or analogues can be administered to compensate for a defective gene, and epithelial cells, or transgenic animals carrying a mutated APC allele are useful for detecting therapeutic agents able to suppress tumorigenesis. (Updated on 25-MAR-2003 to correct PA field.)
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Pred. No. 0;
2; Mismatches
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Best Local Similarity 99.7%;
Matches 2835; Conservative
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Best Local Similarity
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301 PRRLISHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL 360

Adenomatous polyposis coli; tumour repressor; Gardner's syndrome; familial adenomatous polyposis; cancer diagnosis and prognosis; tumorigenesis suppression.

Adenomatous polyposis coli tumour repressor.

(revised) (first entry)

25-MAR-2003 23-MAY-1995

AAR63508;

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AAR63508 standard; protein; 2842

141   PPPGTAGENGENERRESSERIONARIAN/ORDOTESPOLDESCONNERSTEDE   1499     142   PPPGTAGENGENERRESSERIONARIAN/ORDOTESPOLDESCONNERSTEDE   1499     143   PPPGTAGENGENERRESSERIONARIAN/ORDOTESPOLDESCONNERSTEDE   1499     144   PPPGTAGENGENERRESSERIONARIAN/ORDOTESPOLDESCONNERSTEDE   1499     155   MULDOSDODIES   155   155     156   MULDOSDODIES   155   155   155   155     157   MULDOSDODIES   155   155   155   155     158   MULDOSDODIES   155   155   155   155     159   MULDOSDODIES   155   155   155   155     150   MULDOSDODIES   155   155   155   155   155     151   MULDOSDODIES   155   155   155   155   155     152   MULDOSDODIES   155   155   155   155   155     153   MULDOSDODIES   155   155   155   155   155   155     154   MULDOSDODIES   155   155   155   155   155   155     155   MULDOSDODIES   155   155   155   155   155   155   155     155   MULDOSDODIES   155   155   155   155   155   155   155     155   MULDOSDODIES   155   155   155   155   155   155   155   155     156   MULDOSDODIES   155   155   155   155   155   155   155   155     156   MULDOSDODIES   155   155   155   155   155   155   155   155   155     157   MULDOSDODIES   155   155   155   155   155   155   155   155   155   155   155     157   MULDOSDODIES   155   155   155   155   155   155   155   155   155   155   155     157   MULDOSDODIES   155	
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detecting somatic alteration of wild-type adenomatous polyposis coli) protein in a tumour tissue isolated from a human (the alteration indicating neoplasia of the tissue). The method of the invention is useful in diagnosis or prognosis of a neoplastic tissue of a human the method is useful in detection of genetic predisposition to cancer. The present sequence represents a peptide sequence used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELITSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL
                                                                                                                                                                                                                                                                                                          ASSGQIDLLERLKELNIDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 EAERSSQNKHETIGSHDAERQNEGQGVGEINWATSGNGQGSTTRMDHETASVLSSSSTHSA
                                                                                                                                                                                                                  1 MAAASYDQLLKQVEALKGVENSNIRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM
                                                                                                                                                                                                                                                1 MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM
                                                                                                                                                                                                                                                                                                                                          RGPVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL
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                                                                                                                                                                                                                                                                                                                                                                                                                               180 QTDMTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAERSSONKHETGSHDAERONEGOGVGEINMATSGNGQGSTTRMDHETASVLSSSSTHSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLLAMSSSQDSCISMRQSGCLPLLIQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDDKRGRREIRVLHLLEQIRAYCETC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGNDKDSVLLGNSRGSKEARARASAALHNI IHSQPDDKRGRREIRVLHLLEQIRAYCETC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWNLSAHCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QOVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWNLSAHCT
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                                                                                                                                                                                                                                                                                                                                                            121 RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSL-LTENFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 WEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQ
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                                                                                                                                                          DB 5; Length 2842;
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                                                                                                                                                           KTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDN
                      RPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSES
                                           RPAKKHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRTGSSSSILSASSES
                                                                                                 SEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFSPTNSTSQTVSSGATNGAES
                                                                                                                                         KTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDN
                                                                                                                                                                                                                         PFSSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVNNNTKKRDSKT
                                                                               SEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFSPTNSTSQTVSSGATNGAES
                                                                                                                                                                                                     QAKQNVGNGSVPMRTVGLENRLTSFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVERT
                                                                                                                                                                                                                                                                                           PFSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQ1PTPVNNNTKKRDSKT
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, Thliveris A, Vogelstein B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel method to aid in the diagnosis prognosis of a neoplastic tissue of a human. The method involves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APC; human; neoplastic tissue; cancer.
                                                                                                                                                                                                                                                                                                                          DSTESSGTQSPKRHSGSYLVTSV 2843
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Nakamura Y,
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JAPANESE FOUND CANCER RES
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Markham AF,
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16-JAN-1991;
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08-AUG-1991;
12-AUG-1994;
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OY 2761 PFSSSSSKHSSBSGTVAARVIPFNYNPSPRKSSADSTSARPSQIPTPVANNTKKRDSKT 2820	RESULT 10 US-08-821-355A-7 ; Sequence 7, Application US/08821355A ; Patent No. 588175 ; GENERAL INFORMATION:	APPLICANT: Barker, Nick  APPLICANT: Clevers, Hans  APPLICANT: Korinek, Vladimir  APPLICANT: Morin, Patrice	APPLICANI: NITZET, Kenneth APPLICANI: Vogelstein, Bert APPLICANT: Sparks, Andrew ITILE OF INVENTION: Beta Catenin, TCF-4, and APC	rievenc Ltd.	SIRALI 1001 G SLIBEL, N.M. CITY: Washington STATE: DC COUNTRY: USA	COMPUTER READABLE FORM:  HEDIUM TYPE: Diskette  COMPUTER: IBM Compatible	; OPERATING SYSTEM: DOS ; SOFTWARE: FastSEQ for Windows Version 2.0 ; CURRENT APPLICATION DATA: ; APPLICATION UMBER: US/08/821,355A	FILING DAILS - 20-704X-199/ CLASSIFICATION: 514 ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER:	TILITY DATE: TATORNEY SATE: NAME: Kagan, Sarah A REGISTRATION NUMBER: 32,145		INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: TURNETH: 2973 amino acids	NDEDNESS NOGY: 1: LOGY: 1:	Ouery Match  Query Match  Query Match  Best Local Similarity 99.8%; Score 14533; DB 2; Length 2973;  Matches 2836; Conservative 2; Mismatches 5; Indels 0; Gaps 0;	LKQVEALKWENSNLRQELEDNSNHLTKLETERSNMKEVLKQLQGSIEDERM 60 LKQVEALKWENSNLRQELEDNSNHLTKLETERSNMKEVLKQLQGSIEDERM 60 LKQVEALKWENSNLRQELEDNSNHLTKLETERSNMKEVLKQLQGSIEDERM 60	MGSFPR	121 RGFVNGSRESTGYLBELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL

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REGISTRATION NUMBER: 32,145
REGISTRATION NUMBER: 32,145
REFERENCE/DOCKET NUMBER: 1107.05064
TELECHNUNICATION INFORMATION:
TELEFRAX: 202-508-9100
TELEFAX: 202-508-929
TELEFAX: 202-508-929
TELEX: 97430 BMB UT
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2973 amino acids
                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5998600e
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Best Local Similarity 99.8%;
Matches 2836; Conservative 2
       NAME: Kaga
REGISTRATIC
REFERENCE/I
FILEPONE
TELEPA: 2
TELEPA: 974
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                    GOPKPILOKOSTFPOSSKDIPDRGAATDEKLONFAIENTPVCFSHNSSLSSISDIDOENN
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RESULT 12
US-09-136-605-7
Sequence 7, Application US/09136605A
Patent No. 6140052
GENERAL INFORMATION:
APPLICANT: He, Tong-Chuan

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Pred. No. 0;
2; Mismatches
APPLICANT: Kinzler, Kenneth
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Beta Catenin, TCF-4, and
TITLE OF INVENTION: Perevent Cancer;
FILE REPERENCE: 1107.75741
CURRENT APPLICATION NUMBER: US/09/136,605A
CURRENT PILING DATE: 1998-08-20
EARLIER APPLICATION NUMBER: 08/821,355
EARLIER PILING DATE: 1997-03-20
EARLIER PILING DATE: 1997-03-20
FARLIER PILING DATE: 1998-01-06
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
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Best Local Similarity 99.8%;
Matches 2836; Conservative
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8 4 .	PRASHRSKQRAKQSLYGDYVFDINKHDDNRSDNFNTGNMIVLSPYLLNITVLFSSSSSKGS 84 LDSSRSEKDERLERERGIGLGNYHPATENPGTSSKRGLOISTTAAOIAKVMEEVSAIHTS 90	SESSENTELENCYTDERNALDEN THE ALTEN FOLSSENCE LOUGH STANDALLAN VINEEVSALLT.  RESCOTTELENCYTDERNALDEN SAAAHTHSNYTYNFTKSENSNRTCSMYAKLEYRRS.  I	NDSLNSVSSNDGYGKRGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGE 10	INDEPENDENCY COORDES CANAGE AND THE PROPERTY OF THE PROPERTY O	STDDKHLKFOPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSINIFVIIE 100	SIDSKHIRK QFARGQQECVSFIRSKGANGSBINKVOSNHGIRQVAQQSDCQEDDIEDDKFILL INVSERYSEEEQHEEERPINYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSKS 12 "WYTRYGTYGTEFFFIREFFFIREFFILM"	SSGGSSKTEHMSSSSENTSTPSSNAKRONGLHPSSAGSRSGGOOKAATCKVSSINGETIO 12	SGGGSSKIEHMUSSSERISIPSSKARKUNGLHFSSAUGREGGFGRAAICKVSSINGEIIG I26 TYCVEDTPICFSRCSSISSISSAEDEIGCNOTTGEADSANTLGIAEIKGKIGTRSAEDPV 132 TYCVEDTPICFSRCSSISSISSAEDEIGCNOTTGFADSANTLGIAEIKGTRGARDPV 132 TYCVEDTPICFSRCSSISSISSAEDEIGCNOTTGRASSANTLGIAEIKFKTGTRSARDPV 132	SEVPAVSOHPRIKSSRLOGSSLSSESARHKAVEFPSGAKSPSKSGAQIPKSPPEHVVOET 138		PPPQTAQTKREVPKNKAPTAEKRESGPKQAANNAAVQRVQVLPDADTLLHTATESTPDGF 150	SCSSSILATION OF THE CONTROL OF THE C	COCCOSDINISTED INTERPORTED FOR THE SECONDARY OF THE SECON	EGVRGGAQ 168	VANDAY VANDAY ON THE STATE OF T	SOS-ENCOTE FIGURE JEBAÇONISS (TELEBERNANDES) LIBECTUS PREPARADONO PROVINCIA DE L'INTERNANDA PRODUCTION DE L'INTERNANDA PRODUCTION DE L'INTERNANDA PROVINCIA DE L'INTERNANDA PR	AERVFSDNKDSKKONLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRND 186

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Patent No. 5352775

GREBEAL INFORMATION:
APPLICANT: ALBERTSEN, HANS
APPLICANT: ANAND, RAKESH
APPLICANT: GRALSON, MARY
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: HEDGE, RENNETH
APPLICANT: WARKHAM, ALEXANDER F.
APPLICANT: WARKHAM, ALEXANDER F.
APPLICANT: HIJVERIS, MANDEW
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
ITLLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 94
CORRESPONDENCES: 94
CORRESPONDENCES: BAINEY, BICCH, MCKIE & BECKELL
STREET: 1001 G Street: NW
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,940
FILING DATE: 19920109
CLASSIFICATION: 435
ATTONNEY/AGENT INPORMATION:
NAME: REGISTRATION NUMBER: 32,141
REFERRENCE/POCKET UNBER: 32,141
REFERRENCE/POCKET UNBER: 1107.035574
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Pred. No. 0;
2; Mismatches
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TELEPAX: 202-608-9299
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 99.7%;
Matches 2835; Conservative
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STRANDENNESS: single
TOPOLOGY; linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CLONE: APC
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TYPE: AN
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	RESULT 14 US-08-28-548A-7 IS-08-28-28-28-2 Sequence 7, Application US/08289548A Fatert No. 5648212 FATER NO. 5648212 APPLICANT ANNUD FAKESH APPLICANT GRODEN, WAXY APPLICANT GRODEN, WAXY APPLICANT GRODEN, WANT APPLICANT GRODEN, WANT APPLICANT HENGE, PHILIP U. APPLICANT HENGE, PHILIP U. APPLICANT HENGE, PHILIP U. APPLICANT HENGE, PHILIP U. APPLICANT MAXAMURA, ALEXANDER P. APPLICANT MAXAMURA, ALEXANDER P. APPLICANT MAXAMURA, ALEXANDER P. APPLICANT MAXAMURA, ALEXANDER P. APPLICANT MAXAMURA, ALEXANDER P. APPLICANT MAXAMURA, ALEXANDER P. APPLICANT MAXAMURA, ALEXANDER P. APPLICANT MAXAMURA, ALEXANDER P. APPLICANT MAXAMURA, ALEXANDER P. APPLICANT MAXAMURA, ALEXANDER P. APPLICANT MAXAMURA, ALEXANDER P. COUNTRY: Washington GENES: ADDRESSEE: Banner & Allegretti, LTD COUNTRY: U.SA COUNTRY: U.SA COUNTRY: U.SA COUNTRY TEB: R. P. COMPAILE COMPUTER TIPE R. P. COMPAILE COMPUTER TIPE R. P. COMPAILE COMPUTER TIPE R. P. COMPAILE COMPUTER TIPE R. P. COMPAILE COMPANY STERM C. P. COMPAILE COMPANY MARKER WASHINGTON: 435 ACTIONS DATE: L2-SAID MAXAMURA MAXA
1381 PLWESRCTSVSSLDSFESRSIASSVQSEPCSGWVSGIISPSDLPDSPGGTWPPSRSKTPP 1440 1380 PLMFSRCTSVSSLDSFESRSIASSVQSEPCSGWVSGIISPSDLPDSPGGTWPPSRSKTPP 1439 1441 PPPQTAQTKREVPKWAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGF 1500 1440 PPPQTAQTKREVPKWAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGF 1499 1501 SCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSE 1560 1500 SCSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSE 1559 1561 KDLLDDSDDDDIEILEECIISAMPTKSSRKGKKPAQTASKLPPPVARKPSGLPVYKLLPS 1620 1662 QNRLQPQKHVSFTPGDDMFRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 1679 1661 QNRLQPQKHVSFTPGDDMFRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 1679 1661 SGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKP 1740 1680 SGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKP 1739 1741 FRVKKIMDQVQQASASSSAPNKQQLDGKKKKPTSPVKPIPQNTEYRTRVRKMADSKANLN 1800 1740 FRVKKIMDQVQQASASSSAPNKQQLDGKKKKPTSPVKPIPQNTEYRTRVRKMADSKANLN 1799	1801 AERVESDIKOSKKONLKANSKDFNDKLPNNEDRVRGSPAFDSPHHYTPIEGTPYCFSRND 1860 1800 AERVESDIKOSKKONLKANSKDFNDKLPNNEDRVRGSPAFDSPHHYTPIEGTPYCFSRND 1869 1861 SILSSLDFDDDDVDLSREXAELRKAKENRESBAKYTSHTELTSNOQSANKTOALAKOPINR 1920 1860 SLSSLDFDDDDVDLSREKAELRKAKENRESBAKYTSHTELTSNOQSANKTOALAKOPINR 1919 1921 QQPK71LQKQSTFPQSSKDIPDRGAATDEKLQNAALBYTPVCFSHNSSLSSLSDIDOENN 1979 1920 QQPK71LQKQSTFPQSSKDIPDRGAATDEKLQNAALBYTPVCFSHNSSLSSLSDIDOENN 1979 1921 QQPK71LQKQSTFPQSSKDIPDRGAATDEKLQNAALBYTPVCFSHNSSLSSLSDIDOENN 1979 1920 WIGNEPIKETEPPDSQGBPSKPQASGYAPKSFHVEDTPVCFSHNSSLSSLSDIDOENN 1979 1980 NKENEPIKETEPPDSQGBPSKPQASGYAPKSFHVEDTPVCFSHNSSLSSLSDIDOENN 1979 1981 NKENEPIKETEPPDSQGBPSKPQASGYAPKSFHVEDTPVCFSHNSSLSSLSDIDOENN 1979 1980 NKENEPIKETEPPDSQGBPSKPQASGYAPKSFHVEDTPVCFSHNSSLSSLSDIDOENN 1979 1981 NKENEPIKETEPPDSQGBPSKPQASGYAPKSFHVEDTPVCFSHNSSLSSLSDIDOENN 1979 1980 NKENEPIKETEPPDSQGBPSKPQASGYAPKSFHVEDTPVCFSHNSSLSSLSDIDOENN 1979 1980 NKENEPIKETEPPDSQGBPSKPQASGYAPKSFHVEDTPVCFSHNSSLSSLSDIDOENN 1979 1980 NKENEPIKETEPPDSQGBPSKPQASGYAPKSFHVEDTPVCFSHNSSLSSLSDIDOENN 1979 1980 NKENEPIKETEPPDSQGBPSKPQASGYAPKSFHVEDTPVCFSHNSSLSSLSLSDIDOENN 1979 2041 ECISSAMPKKKFSRLKGDNEKHSPRNMGGILGEDLIDLKDIQRPPSEHLFPDQEKKFFT 2159 2100 WKAJQEGANSIVSSLHQAAAACLSRQASSSBSDILGLKSGFFHLTPPQEKKFFT 2159 2161 SNKGPRILKPGEKSTLETYKLESESKGIKGGKKVYKSLITGKYRSNSEISGQWKQPLQAN 2219 2221 MMSIGSGRAFHILFFTKKIESESKGIKGGKWYYKSLITGKYRSNSEISGQWKQPLQAN 2219 2222 NKGPRILKPGEKSTLETYKLESESKGIKGGKWYYKSLITGKYRSNSEISGQWKQPLQAN 2219 2222 NKGPRILKPGEKSTLETYKLESESKGIKGGKWYYKSLITGKYRSNSEISGQWKQPLQAN 2219 2224 NKGSPRILKPGTRYNSSSSTSPYSKKGPPLKTPARAKSSPEGGAPKSPWKS 2279 2225 NKGSPRILKPGTRYNSSSSTSPYSKKGPPLKTPARAKSSPEGGAPKSPWKS 2219 2226 ELSPVARQTSQLGGSSKAPSRGSRSPPRQQDLSRPIQSPRNSISPGRNSISPGRNSISPPRAGGSSPARS 2230 NKGSPRILKPGTRYNSSSSTSPYSKKGSPPRAGGSPRASSSSTSTTLRKATEBESA 2460 2240 LINQWNNGNGANKKVELSENSTYSSGGSBDRSERPVUNGGSRAPSSSR 2459 2401 LINQWNNGNGANKKVELSENSTYSSGGSBDRSERPVUNGGSRAPSSSR 2459 2402 LINGWNNGNGANKKVELSENSTYSSGGSBDRSERPVUNGGSTFIRKBESSA 2440 2402 LINGWNNGNGANKKVELSRSSTXSSGSSBDRSERPVUNGGSTFIRKBESSA 2440 2

EDRSSGSTTELHCVTDERNALRRSSAAHTHSNITNFTKSENSNRTCSMPYAKLE EDRSSGSTTELHCVTDERNALRRSSAAHTHSNITNFTKSENSNRTCSMPYAKLE EDRSSGSTTELHCVTDERNALRRSSAAHTHSNITNFTKSENSNRTCSMPYAKLE DSLNSVSSNDGVGKRGQNKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHND	020 LDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHIIEDEIKQSEGRQSRNQSTTYPVYTE 107	STDDKHLKEQPHFGQQBCVSPYRSRCANGSBTNRVGSNHGINQNVSQSLCQBDDYBDDKP 113	41 TNYSERYSEEQHEEERRTNYSIKYNEERRHVDQPIDYSLKYATDIPSSQXQSFGFSKS 120 	01 SSGQSSKTEHMSSSSENTSTPSSNAKRONQLAPSSAQSRSGOPQKAATCKVSSINOBTIQ 126 	TYCVEDTPICFSRCSSLSSLSSAEDBIGGNQTTQEADSANTLQIABIKGKIGTRSAEDPV 132	21 SEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFPSGAKSPSKSGAQTPKSPPEHYVQET 138	1 PIMFERCISVSSLDSFESRSIASSVQSEPCSGWVSGIISPSDLPDSPGQTMPPSRSKTPP 144	PPPQTAQTKREVPKNKAPTABKKESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGF 1 	1 SCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESBQPKESNENQEKEAEKTIDSE 156	KOLLDDSDDDDIEILEECIISAMPTKSSRKGKKPAQTASKLPPPAARKPSGLPVYKLLPS 162	QNRLQPQKHVSFTPGDDMPRYYCVEGTPINFSTATSLSDJTIESPPNBLAAGEGYRGGAQ 168 	SGEFEREDTIFTEGRSTDEAGGGKTSSVTIFELDDNKAEEGDILAECINSAPKGKSHKP 174 [	KROLDGKKKKPTSPVKEIPONTEYRTRYRKNADSKNNLN 180 	1801 AERVFSDNKDSKKQNLKANSKDFNDKLPNNEDRVRGSFAPDSPHYTPIEGTPYCFSRND 1860 	1861 SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQPINR 1920 	1921 GQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSDIDQENN 1980 
8 8 8 8 8	7 A &	S 8	B Ó	Qy Dp	QY Dp	y d	QY Dp	δλ Dp	VQ DP	yo D	දු දු	පි රි	λ O	P &	VQ QQ	& <u>8</u>
	Query Match 99.6%; Score 14515.5; DB 1; Length 2842; Best Local Similarity 99.7%; Pred. No. 0; Matches 2835; Conservative 2; Mismatches 5; Indels 1; Gaps 1;	Qy 1 MAAASYDQLLKQVEALKYENSNIRQELEDNSNHLTKLETEASNMKEVILKQLQGSIEDEAM 60	Qy 61 ASSGQIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR 120	Qy         121 RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL 180           Db         121 RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSL-LTENFSL 179	OSCAT 	SSTHSA 30	PLLIQLL 3         PLLIQLL 3	AAYCETC 4	WEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSPDEEHRHAMNELGGLQAIAELLO 	VDCEMYGLTNDHYSITLERYAGMALTNLTFGDVANKATLCSMKGCMRALVAQLKSESEDL 	QY 541 QQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWNLSAHCT 600	Qy 601 ENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRENN 660	HKMIAM 7        HKMIAM 7	721 GSAAALRNIMANRPAKKKDANIMSPGSSLPSLHVRKOKALEAELDAQHLSETFDNIDNLS	720 GOARGENEEREN FORTEN NAMED BEGEN FOR GOOD FOR THE STANDARD OF THE STANDARD	841 LDSSREKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTS 90

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180 QTDMTRRQLEYBARQIRVAMESQLGTCQDMEKRAQRRIARIQQIBKDILRIRQLLQSQAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ASSGOIDLLERLKEINLDSSNFPGVKLRSKMSLRSYGSREGSVSRSGECSPVPMGSFPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKAWIRA, YUSUKE
APPLICANT: FILLIVERIS, ANDREM
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE BADNERS:
ADDRESSEE BADNER, Birch, McKie & Beckett
STREET: 1001 G Street, NW
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAPPLICATION DATA:
APPLICATION NUMBER: US/08/452,654
FILING DATE: 25-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/741,940
FILING DATE: US -MAY-1995
ATTORNEY/AGENT INFORMATION:
REJECOMMUNICATION INFORMATION:
NAME: KAGAN, SATA A.
REJECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INF
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ORIGINAL SOURCE:
ORGANIEM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2842 amino ac
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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2760 PFSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVNNNTKRDSKT 2819
             2040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLSQLPRTSSPSTASTKSSGSGKMSYTSPGRQMSQQNLJKQTGLSKNASSIPRSESASKG 2399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2459
                                                       NKENEPIKETEPPDSGGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQ 2039
                                                                                                                                                                                  2040 ECISSAMPKKKKXPSRLKGDNEKHSPRNWGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2099
                                                                                                                                                                                                                                                                                                                2100 WKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKKSGISLGSPFHLTPDQEEKPFT 2159
                                                                                                                                                                                                                                                                                                                                                                                                                                              2160 SNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQPLQAN 2219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2220 MPSISRGRIMIHIPGVRNSSSSISPVSKKGPPLKIPASKSPSEGQIATISPRGAKPSVKS 2279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGRNGISPPN 2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INOMNNGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQSTFIKEAPSPTLRRKLEESA 2460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2461 SFESISPSSRPASPTRSQAQTPVLSPSIPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDG 2520
                                                                                                                                           ECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2100
                                                                                                                                                                                                                                                                                                                                                                                                           SNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQPLQAN 2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MPSISRGRTMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGQTATTSPRGAKPSVKS 2280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGRNGISPPN 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INOMNNGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQSTFIKEAPSPTLRRKLEESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2580 SEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFSPTNSTSQTVSSGATNGAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTLIYQWAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2700 QAKQNVGNGSVPMRTVGLENRLNSFIQVDAPDQKGTEIKPGQNNPVPVSETNBSSIVERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLSQLPRISSPSIASIKSSGSGKMSYISPGRQMSQQNLIKQIGLSKNASSIPRSESASKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTLIYOMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QAKQNVGNGSVPMRTVGLENRLTSFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVERT
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             NKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQ
                                                                                                                                                                                                                                                                             WKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPFT
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US-08-422-654-7
Sequence 7, Application US/08452654
Patent No. 5691454
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, HANS
APPLICANT: CALSON, MARY
APPLICANT: CALSON, MARY
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: USSLYN, GEOFF
APPLICANT: KINZLER, KENNETH
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2641 KTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDN 2700
2640 KTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDN 2699
                                                                                                                                                                                                                                                         2701 QAKQNVGNGSVPMRTVGLENRLTSFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVERT 2760
2520 RPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSES 2579
                                                      2581 SEKAKSEDEKHVNSISGIKQSKENQVSAKGIWRKIKENEFSPINSISQIVSSGAINGAES 2640
                                                                                                  2580 SEKAKSEDEKHVNSISGIKQSKENQVSAKGTWRKIKENEFSPINSTSQIVSSGAINGAES 2639
                                                                                                                                                                                                                                                                                          2700 QAKQNVGNGSVFMRTVGLENRINSFIQVDAPDQKGTEIKPGQNNPVFVSETNESSIVERT 2759
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Search completed: August 25, 2004, 17:25:42 Job time : 53.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 25, 2004, 17:06:26 ; Search time 59 Seconds (without alignments) 4635.127 Million cell updates/sec

Title: Perfect score:

US-09-442-489F-7 14566 1 MAAASYDQLLKQVEALKMEN......ESSGTQSPKRHSGSYLVTSV 2843 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		*			SOUTHWEST	
Result No.	Score	Query Match	Length	DB		Description
1	45	: ;	84		RBHUAP	adenomatous polypo
7	13178	•	84	N	a	adenomatous polypo
m	512	4.	27	7	025	OΩ
4	780	N.	41	7	382	
Ŋ	649	•	32	7	T13564	microtubule-associ
v	517	3.5	2271	7	9007	hypothetical prote
7	513	٠	23	7	T34434	hypothetical prote
œ	11	•	18	7	332	adenomatous polypo
σ	509.5		18	~	T23330	hypothetical prote
10	476	3.3	77	7	335	microtubule-associ
11	454		50	0	_	hypothetical prote
12	453	3.1	77	7	$\sim$	
13	426.5	2.9	1791	Ŋ	T02345	hypothetical prote
14	420		93	N		
15	417.5		72	N	m	hypothetical prote
16	415.5		73	N	$\sim$	protein F07A11.6 [
17	409		94	7	T42730	
18	405.5	2.8	48	N	141	tical prot
19	405		18	7	N	nascent polypeptid
20	404		89	0	947	alpha-A-crystallin
21	400	2.7	52	7	53	hypothetical prote
22	399		92	N	3743	٠.
23	395.5		18	Ġ	C583	걾
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378.5	376.5	375.5	374	372	371.5	370.5	370	369	367	367	365	364.5
30	32 33	3.4	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

A;Residues: 1-2843 <KIN>
A;Cross-references: GB:M74088; NID:g182396; PIDN:AAA05586.1; PID:g182397
A;Cross-references: GB:M74088; NID:g182396; PIDN:AAA05586.1; PID:g182397
R;Joslan, G:, Carlson, M.; Thliveris, A.; Albertsen, H.; Gelbert, L.; Samowitz, W.; Grodk arrington, G.; McPharson, J.; Wasmuth, J.; Le Paslier, D.; Abderrahim, H.; Cohen, D.; Lef Cell 66, 601-613, 1991
A;Title: Identification of deletion mutations and three new genes at the familial polypos A;Accession: B39658; MUD:g133307; PMID:1678319

A; Molecule type: DNA

A; Molecule type: DNA

A; Residues: 1-183, 15.,185-969, N, 971-1308, 'G',11310-1324, 'SS',11326, 'HSTLE', 1332-1354, 'P',

A; Residues: 1-183, 'L', 185-969, ND: 1910163; PIDN: AAA60354.1; PID: 1910164

R; Miki, Y.; Nishisho, I.; Horii, A.; Miyoshi, Y.; Utsunomiya, J.; Kinzler, K.W.; Vogelste R; Miki, Y.; Nishisho, I.; Horii, A.; Miyoshi, Y.; Utsunomiya, J.; Kinzler, K.W.; Vogelste R; Miki, Y.; Distruction of the APC gene by a retrotransposal insertion of L1 sequence in a cc A; Reference number: A44928; MUID: 92119623; PMID: 1310068

A;Accession: A44928
A;Rolecule type: DNA
A;Residues: 1506-1525 <MIK>
A;Cross-references: GB:S78214; NID:g243541; PIDN:AAB21145.1; PID:g243542
A;Cross-references: GB:S78214; NID:g243541; PIDN:AAB21145.1; PID:g243542
A;Note: sequence extracted from NCBI backbone (NCBIN:78214, NCBIP:78218)
R;Spirio, L.; Olschwang, S.; Groden, J.; Robertson, M.; Samowitz, W.; Joslyn, G.; Gelbert Cell 75, 951-957, 1993
A;Title: Alleles of the APC gene: an attenuated form of familial polyposis.
A;Reference number: A49319; MUD:94073973; PMID:8252630
A;Reference number: A49319; MUD:94073973; PMID:8252630

A)Status: preliminary, translated from GB/EMBL/DDBJ
A)Molecule type: mRNA
A,Molecule type: mRNA
A,Rolecule type: mRNA
A,Residues: 'G',143-171,'P', 173-179 <SPI>
A,Cross-references: GB:867787; NID:9461061; PIDN:AAD13997.1; PID:94261697
B,Lambertz, S.; Ballhausen, W.G.
Hum. Genet. 90, 650-652, 1993
A,Title: Identification of an alternative 5' untranslated region of the adenomatous polygangerence number: I54271; MUID:93186137; PMID:8383094

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: 1-4 cLAM>
A;Residues: 1-4 cLAM>
A;Cross-references: GB:SS6365; NID:g266243; PIDN:AAD14918.1; PID:g4262770

191   PRASHERGABHROSLYSDYPDTHRHDDNRSDNFNTGNWTYLSPYLMTTYLPSSSSSRGS 840   1	
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O)	KSESEDL 540  MLSAHCT 600
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GOPKPILOKOSTFPOSSKDIPDRGAATDEKLONFAIENTPVCFSHNSSLSSLSDIDQENN
                  GOPKPILOKOSTFPQSSKDIPDRGAATDEKLONFAIENTPVCFSHNSSLSSLIDGENN
                                                             NKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQ
                                                                                               ECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD
                                                                                                               ECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD
                                                                                                                                                 WKAIQEGANSIVSSLHQAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQBEKPFT
                                                                                                                                                                     WKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPFT
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RESULT 2
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adenomatous polyposis coli protein - mouse
N;Alternate names: APC
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: 149505
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of the R;Su, L.
Science 256, 668-670, 1992
A;Title: Multiple intestinal neoplasia caused by a mutation in the murine homolog of A;Title: Multiple intestinal neoplasia caused by a mutation in the murine homolog of A;Reference number: 149505; MUID:92263101; PMID:1350108
A;Recession: 149505
A;Ratus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2845 of RES
A;Residues: 1-2845 of RES
A;Cross-references: GB:M88127; NID:919991; PIDN:AAB59632.1; PID:91992.
C;Superfamily: adenomatous polyposis coli protein 780 900 10 418 480 478 540 538 600 598 099 658 720 718 778 840 838 120 118 180 178 240 238 300 298 360 358 420 9 9 ENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRENN GSAAALRNIMANRPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLS PKASHRSKQRHKQNLYGDYAFDANRHDDSRSDNFNTGNMTVLSPYLNTTVLPSSSSRGS LDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTS 61 -TSGQIDLLERLKEFNLD-SNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR RIFVNGSRESTGYLEELEKERSLLLADIDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL QTDMTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT QTDMTRRQLEYEARQIRAAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRVRQLLQSQAA PRRITSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL PRRITSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL WEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQ WEWQEAHEQGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQ VDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCSMKGCMRALVAQLKSESEDL CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSKHKMIAM CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSKHKMIAM GSAAALRNIMANRPAKYKDANIMSPGSSLPSLHVRKQKALBAELDAQHLSETFDNIDNLS PKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSSRGS 1 MAAASYDQLLKQVEALKWENSNLRQELEDNSNHITKLETEASNMKEVLKQLQGSIEDETM RGEVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLONLTKRIDSLPLTENFSL EAERSSONKHETGSHDAERONEGOGVGEINMATSGNGOGSTTRMDHETASVLSSSSTHSA HGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDDKRGRREIRVLHLLEQIRAYCETC VDCEMYGLTNDHYSVTLRRYAGMALTNLTFGDVANKATLCSMKGCMRALVAQLKSESEDL QQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALBVKKESTLKSVLSALWNLSAHCT ENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRENN 1 MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM 61 ASSGQIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR Gaps 12; 2845; Length Indels Query Match 90.5%; Score 13178; DB 2; Best Local Similarity 90.2%; Pred. No. 0; Matches 2572; Conservative 111; Mismatches 155; 479 629 599 779 419 481 539 721 719 781 841 121 119 179 241 239 301 299 361 421 541 601 661 181 g 6 음 상 음 <u>ک</u> ۾ ò g ð 8 B 8 셤 8 8 S S S ö g ₹ d ò g à 원 임 ò ઠે

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939 LDSSRSEKDRSLERERGIGLSAYHPTTENAGTSSKRGLQITTTAAQIAKVMEEVSAIHTS 998 901 QEDRSSGSTTELHCYTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS 960	STDDKHLKFOPHFGQDECVSPYRSRCANGSETNRVGSNHGINQNVGGSLCQEDDYEDDKP 114  NTDDKHLKFQPHFGQQECVSPYRSRCANGSETNRWGSSHAINQNVNGSLCQEDDYEDDKP 113  TNYSERYSEEGH-EEEERPTNYSIKYNEEKHVDQPIDYSLKYATDIPSSQQSFSFSK 119  TNYSERYSEEGH-EEEERPTNYSIKYNEEKHVDQPIDYSLKYATDIPSSQQSFSFSK 119  TNYSERYSEEGH-EEEERPTNYSIKYNEEKHVDQPIDYSLKYATDIPSSQQSFSFSK 119  TNYSERYSEEGH-EEEERPTNYSIKYNEEKHVDQPIDYSLKYATDIPSSQQRSFSFSK 119  SSSGQSSKTEHMSSSSENTSTPSSNAKRQNQLHPSSAQSRSGQPQKAATCKVSSINQETI 125:	ETPLMESRCISVSSLOSFESRAIASVOSEPGGGWYSGIISPSDLPDSGGGUNPESRKY ETPLVESRCISVSSLOSFESRAIASVOSEPGGGWYSGIISPSDLPDSGGGUNPESRKY ETPLVESRCISVSSLOSFESRAIASVOSEPGGGWYSGIISPSDLPDSGGGUNPESRKY ETPLVESRCISVSSLOSFESRAIASVOSEPGGGWYSGIISPSDLPDSGGGUNPESRKY ETPLVESRCISVSKWAPTAEKRESGPKQAVNAAVQRVQVLPDADTLLHFATESTPD PPPPPQTAQTKREVPKSKVAPTAEKRESGPKQAVNAAVQRVQVLPDADTLLHFATESTPD GFSCSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPESNENQDKEAEKTID GFSCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPESNENQDKEVERP-D SEKDLLDDSDDDDIEILEECIISAMPTKSSRKAKKPAQTASKLPPPVARKPSQLPVYKLL FILI	1799 LINBERVESDIKUSKKQNI-KANISKOFINKL-PINIEDRYRGSFAFDSPHHTTPIEGTPYGFSR 1858  1797 VINTEETESDIKUSKKPSLQTNAKAFNEKL-PINIEDRYRGFFALDSPHHTTPIEGTPYGFSR 1856  1859 NDSLSSLDFDDDDVDLSREKAFENKESEBAKVTSHTELTSNQQSANKTQATAKQPI 1918
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                                       A;Molecule type: DNA
A;Residues: 1-2274 <VAN>
A;Cross-references: EMBL:AJ130783; NID:g4210431; PIDN:CAA10207.1; PID:g4210432
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                                                                                                                                                                                                                                     ASYEQLVRQVEALKAENTHLRQELRDNSSHLSKLETETSGMKEVLKHLQGKLEQEARVLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSSSSTHSAPRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLLAMSSSQDSCISMRQSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSALWNLSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----VLSPYLNTTVLPSSSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATENPGTSS
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                                                                                                                                                                                                                    ASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEA--MA
                                                                                                                                                                                    Indels 779; Gaps
                                                                                                                                                     DB 2; Length 2274;
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                                                                                                                                                 24.1%; Score 3512.5; DB 2;
ilarity 34.3%; Pred. No. 6.3e-136;
Conservative 354; Mismatches 788;
Accession: T30258; status: preliminary; translated from GB/EMBL/DDBJ.molecule type: DNA
                                                                                                                                                   Query Match
Best Local Similarity
Matches 1005; Conserv
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A.Reference number: A.Accession: 11382: A.Status: prelimina A.Molecule type: mt A.Residues: 12416 A.Cross references: A.Gene: D.APC A.Koss references: A.Map position: 3R	Query Match Best Local Simila Matches 720; Co	243 ERSSC   129 ELREN	296 STHS.     189 APAP	338 SSSQI   : 249 SGNAQ	398 KRGRH             299 KAGRR	456 LSFDE :     350 VSFDE	515 NKATI      410 NKALI	575 CALEV  : 470 AAMRN	635 GGGII         530 AGGII	695 QEALW  :    590 QKFLW	750 PSLHV  :  650 PTLEA	810 RSDNF 678	870 PGTSS	930 THSNI 726 990 DESKE 750 ME
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	QY 2091 GLSPDSENFDWKAIOEGANSIVSSIHQAAAAACISRQASSDSDSILSLKSGISLGSPF 2148	QY 2149 HLTPDQEEKPFTSNKGPRILKPGEKSTLETKKI-ESESKGIKGGKKVYKSLITGKVR-SN 2206  DD 1702 QPSKLRKGRKPAAEAGGAWRPEKRGTTSTKINGSPRLPN 1740	OY 2207 SEISGOMKOPLOANMPSISRGRTMIHIPGVRNSSSTSPVSKKGPPLKTPASKSPSEGOT 2266  Db 1741 GPEKAKGTOKAMAGESTMIRGRTVIYSAGPASRTOSKGISGPCTTPKKTGTS 1792	QY 2267 ATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQPLSRPIQSPGR 2326	QY 2327 NSISPGRNGISPPNKLSQLPRTSSPSTASTKSSGSGKWSYTSPGRQWSQQN 2377	QY 2378 LIKQTGLSKNASSIPRSESASKGLNQMNNGNGA-NKKVELSRMS 2420  1888 LAKQHKIQKSPVRIPFWQRPARRVPPPLARPSPEPGSRGRAGAEGTPGARGSRLGLVRMA 1947	QY 2421 STKSSGSESDRSERPVLVRQSTFIKEAPSPTLRRKLBESAAFESLSPSSRPASPTRSQAQ 2480   :         :	QY 2481 TPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPS 2537	QY 2538 RLPINRSGTWKREHSKHSSLERVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSIS- 2596	Qy 2597 -GTKQSKENQVSAKGTWRXIKENEFSPTNSTSQTVSSGATNGAESKTLIYQMA 2648	QY 2649 PAVSKTEDVWYRIEDCPINNFRSGRSPTGNTPPVIDSVSEKANPNIKDSKDNQAKÇNV 2706	Qy 2707 GNGSVPWRTVGLENRLNSFIQVDAPDQKGTEIKPGQNNPVPVSETNESSIVERTPFSSSS 2766  Db 2189ASGPVAPQGSDVDGPVLTKPPASAPFPHEGLSAVIAGFP 2227	Qy 2767 SSKHSSPSGTVAARVTPPNYNPSPRKSSADSTSARPSQIPTPVN 2810 	RESULT 4  T13825 adenomatous polyposis coli protein - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Species: O-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000 C;Accession: T13825 R;Hayashi, S; Rubinfeld, B; Souza, B; Polakis, P; Wieschaus, E; Levine, A.J. Proc. Natl. Acad. Sci. U.S.A. 94, 242-247, 1997 A;Title: A Drosophila homolog of the tumor suppressor gene adenomatous polyposis coli dd

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                                                                                        s: EMBL:U77947; NID:g1800228; PID:g1800229; PIDN:AAB41404.1
                                                                                                                                                                                                                                                                                               SAPR------RLTSH-----RGTKVEMVYSLLSMLGTHDKDDMSRTLLAM
                                                                                                                                                                                                                                                                                                                                                                    BEHRHAMNELGGLQAIAELLQVDCEMYG-LTNDHYSITLRRYAGMALTNLTFGDVA
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                                                                                                                                                                                                                                                                                                                                                                                                                       DOSCISMROSGCLPLLIQLLHGNDKDSVLLGNSRGSKBARARASAALHNIIHSOPDD
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                                                                                                                                                                                                Length 2416;
                                                                                                                                                                                                12.2%; Score 1780.5; DB 2; Length larity 25.4%; Pred. No. 5.3e-65; Conservative 329; Mismatches 847; Indels
Z17782; MUID:97144426; PMID:8990193
                                    lary; translated from GB/EMBL/DDBJ
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1509KSKEPSRRESIAESLKAESTKDEKSAPPSKEASRPGSVVESVKDETEKS 1557 760 LEAELDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNM 819	87	873 SSKRGLQISTTAAQIAKYMEEVSAIHTSQEDRSSGSTTELHCVTDERNALRRSSAAHTHS 932 	933 NTYNFTKSENSNRTCSMPYAKLEYKRSSNDSLNSVSSSDGYGKRGQMKPSIESYSED 989  ;	990 DESKFCSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNS 1038 :	1039GRQSPSQNERWARPKHIIEDEIKQSEQRQSRNQSTTYPVYT 1079 	1080 ESTDDKHLKRQPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQE 1132	1133 DDYEDDKPTNYSERYSEE-EQHEEERPTNYSIKYNEEKRHVDQPIDYSLKXATDIP 1188 1934 SPLPSKEASRPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEASRPASVA 1985	1189 SSGKQSFSFSKSSSGQSSKTEHMSSSSENTSTPSSNAKRQNQLHPSSAQSRS 1240	1241 GQPQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSLS-SAEDEIGC 1289	1290 NQTTQEADSANTLQIABIKEKIGTRSAEDPVSEVPAVSQHPRTKSSRLQG 1339 1:::	1340 SSLSSESARHKAVEFSSGAKGPSKS-GAQTPKSPEHYVQETPLMFSRCTSVSSLDSFES 1398	1399 RSIASSVQSEPCSGMVSGIISPSDLPD-SPQCTMPP-SRSKTPPPPPQTAQTKR 1450 :	1451 EVPKN-KAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPD 1498 2251 ESIAESIKASSPRDEKSPLASKEASRPGSVAESIKYDLDKPQIIKDDKSTEHSRRESLED 2310	1499 GFSCSSSL8 1507 : :	1508	1526	1570 DDIBILEBCIISAMPTKSSRKAKKPAQTASKLPPPVARKPSQLPVYKL 1617 
8 8 8	S dd	ර් යි	\$ Q	& A	\$ A	\$ B	යි යි	SP 65	& A	ර් සි	\$ B	\( \frac{1}{2} \)	\$ A	S G	\$ B	\$ A	& <del>4</del>
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A;Accession: T13564 A;Status: preliminary; translated from GB/EWBL/DDBJ A;Molecule type: DNA A;Residues: 1-5327 <spa> A;Cross-references: EWBL:AL031128; PIDN:CAA20006.1</spa>	<pre>is-references: FlyBase:FBgn0025392 is-references: 24/2; 52/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5272/1 is-GG-49E4.1 refamily: Drosophila 576K microtubule-associated protein homolog</pre>	ingth 5327; Indels 968:	15 ALKWENSNLRQELE-DNSNHLTKLETEASNMKEVLKQLQGSIEDEAMASSGQIDLLERLK		EMPAEGICUGENEPDEEBESTLILEKEEVEQYTEDSIVEQESSMIKE	ENFSLOTDWIRRQLEYEARQIRVAMEBOLGTCODMEK-RAQRRIAR	EGASARQDESELDVEPEQSKIKAEVQDIIATAKDIAKSRTEEQLAKPAEEELSSPTPEEK IQQIEK :   ::	LSKKTSDTKODQIGAPVDVLPVNLQESLPEEKFSATIESGATTAPTLPEDERIPLDQIKE  DILRIRQLLQSQATEAERSSQNKHETGSHDAERQNEGQGVGEINM   :: :: : : : :       : : : :     : : :     : : :     : : : :     : : :     : : : : :     : : : :     : : : : :     : : : : :     : : : : : :     : : : : : : : :     : : : : : : : : : : : : : : : : :     :	1082 DLVIEEKYVKEETKEAEAIVVATVQTLPEAAPLAIDTIILABATKDAPKDANAEALGE-L 1139 272 ATSGNGQGSTTRMDHETASVLSSSSTHSAPRRLTSHLGTKVEMVYSLLSMLGTHDK 327 1110 BISCH	DDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLLHGNDKDS	1187 DSQDANAKSISHKEBSAKEEKETDDEKENKVGEIELGDEPNKVDISHVLLKESVQEVAEK 1246 368 VLLGNSRGSKEARAPASAALHNIIHSQPDDKRGRREIRVLHLLEQIRAYCETCWEWQEAH 427 10.1	OICPAVCVLMKLSFDEEHRHAMN	ELGGLQAIAELLQVDCEMYGLTNDHYSITLRRYAGMALTNLFGDVANKATLCSMKG	1341 DTGSIESPPTIEEAIEVE 1358  525 CMRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVK-KES 583  13.50	TLKSVLSALWNLSAHCTENKADICAVDGALAFLUGTLTYRSQTNTLAIIESGGGILRNVS	644 SLIATNEDHRQILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWD 700	SIANIENLESSLENANGERSKESLENGESINERSAFLEASEERSKESVILD MGAVSMLKNLIHSKHKMIAMG-SAAALRNLMANRPAKYKDANIMSPGSSLPSLHVRKQKA

Oy 2539 LPINRSG ' Db 3502	Qy 2599 KQSKENQ :  : Db 3553 EASRPAS	2650	Db 3610 EVSRRES	3651	OY 2770 HSSPSGT : : : : Db 3705 PTSVAES	2822	Db 3764 SMPESG	RESULT 6 F90073	hypothetical protein C,Species: Staphyloco	C;Date: 10-May-2001 # C;Accession: F90073 R;Kuroda, M.; Obta, T	ma, A.; Mizutani-Ui, C.; Shiba, T.; Hatto	A;Title: Whole genome	A, Accession: F90073 A; Status: preliminary	A; Molecule type: DNA A: Residues: 1-2271 <	A,Cross-references: C,Experimental source	A;Gene: SA2447	Query Match Best Local Similari Matches 450; Cons	Qy 606 ICAVDG	Db 353 IGGLSNZ	Qy 647 ATNEDHI	Db 413 ADNAAKU	QY 707 LKNLIH	Db 462 SGTTNF9	Qy 754 VI	Db 522 QVVTID	Qy 809 NRSDNF1	Db 574 VKAPIV		Db 624 INSIIG
1618LPSQNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELA 1670	DEACGGKTSSVTIPELDDNKAEE	2605 PAESAKDAAESVEKSKDASRPPSVVESTKADSTKGDISPSPESVLEGPKDDVEKSKESSR 2664 1721GDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSA- 1759		1760	DSKNNLNAERVF			1894 VTSHTELTSNQQSANKTQALAKQPINRGQPKPILQKQSTFPQSSKDIPDRGAATD 1948	SIKH-ENTKDEESPLGSRRDSVABSIKSDITKGEKSPLPSKEVSRPESVVGSIKD	1949 EKLONFA IENTPVCFSHNSSISSLSD		2998 DEKSLLVSQEASRPESEAESLKDAAPSQETSRPESVTESVKDGKSPVASKE 3049	2020 CFSRNSSLSSLSIDSEDDLLQECISSAMPKKKKFSRLKGDNEKHSPRNMGGIL 2072	3050 -ASRPASVAENAKDSADESKEQRPESLPQSKAGSIKDEKSPLASKDEAEKSKEESRRESV 3108	2073 GEDLTLDLKDIQRPDS-EHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSD 2131	ABÇI'R DVONE VONERO VABO VADBALITATIONE	2132 SDSILSLKSGISLGSPFHLTPDQBEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGG 2191	ISRGRIMIHIPGVRNSSSSTSPVSK	3192 BSVKDEADKSKEESRRE-SGAEKSPLASKEASRPASVAESIKDEAEKSK 3239	2249 KGPPLKTPASKSPSEGGTATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRD 2306	EESKKESVAEKSYLFOKEA-OKFISVAKSVAUGAENSAAESSANDA VARBABASAESSANDA VARBASAKE	STPSKPAQUPLSKPIQSPGRNSISPGRNGISPPNALSQLFKISSPS.ABSIASSGSGAASI         strandardsbasevereenneense	ASVAESVUDEAEKSKEEGKRESVAEKSPLATKEAVAESTRUDAEKSK	2367 TSPGROMSOONLTKQTGLSKNASSIPRESSASKGLNOMNNGNGANKKVELSKMSSTKSSG 2426 2351 -::::::   :::              :    :  :  :::  3251	VACACA CANADA CA	DESCRIPTION OF THE PROPERTY OF	T C DCT DDWGT CTTLCCT/CAGADYT DDMT.CDMTEVNIAGDDXPHDTAPCHCROPS	DAEKSKEESRRESVAEKSPLASKEASRPASVAESVVDEAEKSKEES 350	
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T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; tori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. 40, 2001
me sequencing of meticillin-resistant Stapylococcus aureus.
A89758; MUID:21311952; PMID:11418146 BDVWVRIEDCPINNPRSGRSPIGNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNG 2709 VGLENRINSFIQVDAPDQKGTEIKPGQNNPVPVSFTNESSIVERTPFSSSSSK 2769 SVAEŠVKDEAEKSKEESRRESVAEKSPLAŠKE---ASRPASVAESVKDEAEKSK 3609 75; QV--SAKGTWRKIKEN-----EFSPINSTSQIVSSGAINGAESKTLIYQMAP 2649 206 GTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGT 2598 <KUR>
GB:BA000018; PID:g13702612; PIDN:BAB43752.1; GSPDB:GN00149
ce: strain N315 808 866 623 GTSSKRGLQISTTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCVTDERNALR-- 923 GTPTKIG------QSTVTVVSTDQANNKSTTTFTINVVDTTAPTVTPI 670 GALAFLVGTLTYRSQTNTLAIIE-----SGGGIL------RNVSSLI 646 753 n SA2447 [imported] - Staphylococcus aureus (strain N315) coccus aureus #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001 HRQILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSM HSKHKMIAMGSAAALRNLM-----ANRPAKYKDA----NIMSPGSSLPSLH -RKOKALEAELDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYVFDTNRHDD FNTGNMTV-LSPYLNTTVLPSSSSSRGSLDSSRSEKDRSLERERGIGLG-NYHPA VTVGNQTIEVGKTMNPVVLTTTDNGTGTVTNTVT-----GLPSGLSYDSA | | | | : | : | : | DNQQSALTAK-----GYNYTSVDSSYASTYNDTNKTVKATNAGQSV--TYYFTD 3.5%; Score 517; DB 2; Length 2271; rity 19.5%; Pred. No. 2.5e-13; nservative 332; Mismatches 1013; Indels 514; Gaps Length 2271; 3 3769

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                                                                                                                                                                                                             2035 EDDLLQECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSP 2094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2212 OMKOPLOANMPSISRGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGOTATISP 2271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLRRKLBESASFESLSPSSRPASPTRSQAQTPVLSPS-LPDMSLSTHSSVQAGGWRKLPP 2509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TSESLSTSMSGSQS--- 2154
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C)Species: Caenorhabditis elegans
C)Species: Caenorhabditis elegans
C)Accession: T34A34
R)Gesiael, C.; Gattung, S.
R)Gesiael, C.; Gattung, S.
R)BL Date to the EMBL Date Library, December 1996
A;Description: The sequence of C. elegans cosmid K06A9.
A;Reference number: Z21525
A;Accession: T34434
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                   -----DSVSDSTS
1976 DQENNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDT-PVCFSRNSSLSSLSIDS
                                                                DSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2630 VS---SGATNGAESKTLIYOMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2331 PGRNGISPPNKLSQLPRTSSPSTASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKNASS
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---SKENQVSAKGTWRKIKENBFSPTNSTSQTVSSGATNGAESKTLIYQMAPAVSKTEDV 2657 2718 LENRLNSFIQVDAPDQKGTEIKPGQNNPVPVSET-NESSIVERTPFSSSSSKHSSPSGT 2776 --TEASSTSGGSSTSPNPSQSTSPSTSGATSSPGSSGTTLTSISPSPSQSSTIGSSQGST 1138 G-----TVGSTISESSTTASASSQTG-STVTWGSSSTSGVSTSASSTQPQMSTS TMSSTSSGTVGSTARSQSSTARASTTSHTGSTVTLGSSSTSSNQMSTSQGSSVGSTVASSTA 2079 DLKDIQRPDSEHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSL QP-----QMSTSQG------SSAGSTVASSTAGLVSTSTVPSSTGTMGSTSS QGSSAGSTVASSTTGLVSTSTVPSSTGTMGSTSSGTVGSTISESSTÄASASSQTGSTVTM TWKREH----SKHSSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQ | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : DSPHHYTPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTEL PSTSQSPNPSTSGSSTP----TPNP---SQSTSPVVS----TTTGEMTSHGSTQTP -----PSSTQSFSSTS-----EGSSKASSSPVPSQTSSTPTNPTGSTESSTL-L TPASKSPSEGOTATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQ QPLSRPIQSPGRNSISPGRNGISPPNKLSQLPRTSSPSTA----STKSSGSGKWSYTSP DRSERPVIVROST ----FIKEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQTPVLS PSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSG WVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNGSVPMRTVG 1961 VCFSHNSSLSSLSDIDQENNNKENEPIKETEPPDSQGE-PSKPQASGYAPKSFHVEDTPV KSGISLGSPFHLTPDQ-----EEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKV YKSLITGKVRSNSEISGQMKQPLQANMPSISRGRTMIHIPGVRNSSSSTSPVSKKGPPLK -----STSSASSTQPQMSTSQGSSAGSTV-----ASSTASPAA----GROMSQONLTKOTGLSKNASSIPRSESASKGLNOMNNGNGANKKVELSRMSSTKSSGSES TSNOOSANKTOALAKOPINRGOPKPILQKOSTFPOSSKDIPDRGAATDEKLONFALENTP STI--GSTVTQPSTVSGSNSSGSTVTIGSSEASTSGSSFKTSPSSISPVPTSSPIPF CFSRN-SSLSSLSIDSEDDLLQECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTL SSTIS-GSTQHTIMSKASSGSTSPSTNSQTGSTVTMGSSST-----SGV----ONTEYRTRVRKNADSKANLINAERVFSDNKDSKKONLKANSKDFNDKLPINNEDRVRGSFAF ----TSTQQSVSTNSPGSTVTQPST----VRGSTSS GDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSAPNKNQLDGKKKKPTSPVKPIP GLVŠTSTVPŠSTČIMGSTSSGTVGSTISESSTTAŠASSQTGSTVĪM-ELAAGEGVRGGAQSGEFEKRDTIP-TEGRSTDEAQGGKTSSVTIPE-GSTVTTGSTEGS-AIS-----1230 1362 2139 2315 2370 2430 1720 2546 1901 1259 1436 2195 2255 1512 1570 1611 1660 2486 2601 1830 2658 1781 1199 2020 1393 1479 1081 1721 1139 1841 1304 임 40 60 60 60 8 8 g ò ð 2075/ 2049/1; 1445 1499 1547 1215 1385 NQEKEAEKTIDSEKDLLDDSDDDDIBILEECIISAMPTKSSRKAKKPAQTASKLPPPVAR 1607 GOMKPSIESYSEDDESKFCSYGOYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQL 1036 ECVSPYRSRGANGSETNRVGSNHGINQNV-SQSLCQEDDYEDDKPTNYSERYSEEEQHEE 1155 ENTS-----TPSSNAKRQNQLHPSSAQSRSGQPQKAATCKVSSINQETIQTYCVEDTP 1268 ICFSRCSSLSSLSSAEDEI---GCNOTTOEADSANTLQIAEIKEKIGTRSAEDPVSEVPA 1325 NSGROSPSQNERWARPKHIIEDEIKQSEQROSRNQSTTYPVYTESTDDKHLKFQPHFGQQ 1096 904 964 A;Molecule type: DNA A;Residues: 1-2232 <GEI> A;Residues: 1-2232 <GEI> A;Cross-references: EMBL:U80846; PIDN:AAC70890.1; GSPDB:GN00028; CESP:K06A9.1a A;Experimental source: strain Bristol N2; clone K06A9 C;Genetics: A;Gene: CESP:K06A9.1a A;Gene: CESP:K06A9.1a A;Map position: X A;Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049 70, SPAPSSSPAPSSSPASTGSTITIS-----GSSSIIVSTVSGST 570 699 707 757 976 527 -----TPGSSSTVPSSSSP 596 VSQHPRTKSSRLQGSSLSSESARHKAVEFSSGAKSPSKSGAQTPKSPPEHYVQETPLMFS RCISVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQT ---AQTKREVPKNKAPTAEKRES-GPKQ--AAVNAAVQRVQVLPDADTLLHFATESTPDG FS------CSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNE KPSQLPVYKLLPSQNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPN TOSSGAQSTLTTPS-----PNPSOSTSSLESSTSGATTSSGSAGTTMTSPSQSSS -----TVLPSSSSRGSLDSSRSEKDRSLERER :||: ::| :: | STGSTVTVAPVSGSSTPTASSSSGGTVTVVSGSSSTTVGS--STPSASSSSAGTAS GIGLGNYHPATENPGISSKRGLQISTTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCVT DERNALRRSSAAHTHSNITYNFIKSENSNRTCSMPYAKLEYKRSSNDSLNSVSSSDGYGKR QPSSQSPAPNTGSTTPS----TPTGSSQSPSPMNPSSS----TPTGSSQ EERPTNYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSKSSSGQSSKTEHMSSSS ----ISPSSSITIGSSQGSTS----584; Query Match
3.5%; Score 513; DB 2; Length 2232;
Best Local Similarity 20.0%; Pred. No. 3.6e-13;
Matches 425; Conservative 251; Mismatches 861; Indels 58 STITPEGSTAS--SPTGSTGSTFSVATEVTSQSTV------NTGNMTVLSPYLNT-----GTSQSTLASSTA---------GTTLTS 815 1037 1386 1500 1156 1216 708 1326 856 905 917 1097 1269 758 857 637 670 416 474 528 977 571 597 813 음 상 음 \$ B \$ 9 9 9 9 8 8 8 8 g 8 S B Q ద 8 ò

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:   :   :   :         :   :         :         :         :         :           :           :		1965 NPSSPRSLSQITITPSPSQSTESTQTSLPSSSPSPSTHSVSSSEGTTMSSGATSGDKMS 2024	ESSGTQSPKRHSGSYLVTS 284	C707		adehomatous polyposis coli protein 1 - Caenorhabditis elegans N'Alternate names: apr-1 protein C'Snerios: Caenorhabditis elegans	.: 15-Oct-109mandris argams : 15-Oct-1099 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 Sasion: 703337: 703822	ner, A. the EMBL Data Library, July 1996	sssion: T23327 us: preliminary; translated from GB/EMBL/DDBJ	equie type: DNA Idues: 1-1186 <wil></wil>	Y.; Cha, Y.H.; A	de: Wnt signaling and an APC related gene specify endoderm in early C. elegans embr erence number: Z15051; MUID:97433081; PMID:9288750	BSB101: 103822 preliminary; translated from GB/EMBL/DDBJ profile trace, mbMs	A.Residues: 1-1186 <roc> A.Residues: 1-1186 <roc> A.Cross-references: EMBL:AF013950; NID:g2338717; PIDN:AAC47747.1; PID:g2338718 A.Experimental source: strain Bristol</roc></roc>	.c.edutics. A.jeduticn: apr-1; CESP:KO4G2.8a A.Map position: 1 A.jeduticn: 51/3; 113/2; 355/3; 551/3; 1161/3	uery match: 3.5%; Score 511.5; DB 2; Length 1186;		271 MATSGNGGGSTTRMDHETASVLSSSSTHSAPRRLTSHLGTKVEMVYSLLSMLGTHDKDDM 330	SRTLIAMSSQDSCISMRQSGCLPLLIQLLHGNDKDSVLLGNSRGSKEARARARALHN-	51 EEHYARFKEDIALEVDDALTVLLSSLHFEHKKULVFTDEDDNKLKELHEK 100 390IIHSOPDDKRGRREIRVLHILEOIRAYCETCWEWOEAHEPCNDODKNPMPAPVEHOI 446		447 CPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQVDCEMYGLTNDHYSITLRRYAGMA 504	505 LTNLTFGDVANKATLCSMKGCMRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLR 564  210 LTNLTYGQIHSKRRLCSYDGFIRCVV-RIVIESPNITQVYAGLIRNLSWNADSGMSEALQ 268	BVGSVKALMBCALBVKKES-TLKSVLSALWNLSAHCTENKADICAVDGALAFLVGTLTYR :	209 FIVHALDSIAAVRAHIRKFUVIAILDSALMNIAGASVENKKIICUTFNCUKVLASLLUSFU 320

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A;Accession: T23330 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule Cype: DNA A;Residues: 1-1188 «WIL» A;Residues: 1-1188 «WIL» A;Cossereferences: EMBL:Z75712; PIDN:CAB00048.1; GSPDB:GN00019; CESP:K04G2.8b A;Genetics: C;Genetics: C;Genetics: CESP:K04G2.8b A;Map position: 1 A;Introns: 61/3; 113/2; 355/3; 551/3; 1069/3; 1163/3	y Match 3.5%; Score 509.5; DB 2; Length 1188; Local Similarity 22.0%; Pred. No. 2.2e-13; Conservative 217; Mismatches 582; Indels 217; Gaps 50;	271 MATSGNGGGSTTRMDHETASVLSSSSTHSAPRRITSHLGTKVEMVYSLLSMLGTHDKDDM 330	331 SRTLLAMSSSQDSCISWRQSGCLPLLIQLLHGNDXDSVLLGNSRGSKEARARASAALHN- 389 	390IIHSQPDDKRGRREIRVLHLLEQIRAYCETCWBWQBAHEPGMDQDKNPMPAPVEHQI 446 101 IFALITSESDVNRKRRLKKALPASNCVREQVYYLRRKPSTPPASYYHRL 149	447 CPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQVDCEMYGLTNDHYSITLRRYAGMA 504	505 LINLIFEDVANKATLCSMKGCMRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLR 564 210 LINLIFYGQIHSKRRLCSYDGFIRCVV-RIVIESPNITQVYAGLIRNLSWNADSGMSEALQ 268	565 EVGSVKALMECALEVKKES-TLKSVLSALMNLSAHCTENKADICAVDGALAFLVGTLTYR 623 :	624 SQTNTLAIIESGGGILRNVSSLIATNEDHRQILRENNCLQTLLQHLKSHSLTIVSNACGT 683 	684 LWNLSARNPKDQBAL-WDWGAVSMLKNLIHSKHKMIAMGSAAALRNLMANRPAKYKDANI 742 :	743 M-SPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYVF 801	802 DINRHDDNRSDNFWIGNMIVLSPYLNTIVLPSSSSRRGSLDSSRSEK-DRSLERERG 857	858 IGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCV 915	916 TDERNALRRSSAAHTHSNITYNFIKSENSNRICSMPYAKLEYRRSSNDSLNSVSSSDGYGK 975 	976 RGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNGELDTPIN 1026	1027 -YSLKYSDEQLNSGRQSPSQNERWARPKHIIEDEIKQSEQRQSRNQS 1072  ::	1073 TYYPVYTESTDDKHLKFQPHFGQQECVSPYRSRGANGSETNRVGSNHGI 1121
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Microbuble-associated protein MAPIA - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 13-Aug-1999
C;Accession: A43359; S22108
R;Langkopf, A.; Hammarback, J.A.; Muller, R.; Vallee, R.B.; Garner, C.C.
J. Biol. Chem. 267, 16561-16566, 1992
A;Title: Microtubule-associated proteins 1A and LC2. Two proteins encoded in one messenge A;Title: Microtubule-associated proteins 1A and LC2. Two proteins encoded in one messenge A;Accession: A43359; MUID:9235629; PMID:1379599
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A;Roicesion: Caracted from NCBI backbone (NCBIN:111039) NCBIP:111040)
A;Cravchik, A.
Submitted to the EMBL Data Library, June 1992
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A;Accession 1228 QNQLHPSSAQSRSGQPQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSLSSAEDEI 1287 1288 GCNQTTQEADSANTLQIAEIKEKIGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSSESA 1347 1348 RHKAVEFSSGAKS----PSKSG------AQTPKSPP-----EHYVQETPLMF 1384 : |: || : || :| 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 || 11 1385 SRCTSVSSLDSFESRS----IASSVQSEPCSGMVSGIISPSDLPDSP--GQTMPPSR 1435 1098 ------DSIENQTRDDTIYVNAPVVEAEQERIYMMALKQQKNIEQSPSIGNGSPIAK 1148 1122 NONVSOSLCQEDDY-----EDDKPINYSERYSEEEQHEEEERPINYSIKYNEEKRHVD 1174 1175 -----QPIDYS-LKYATDIPSŞQKQSFSFSKSSSGQSSKTEHMSSSSENTSTPSSNAKR 1227 649 700 701 MGAVSM--LKNLIHSKHKMIAMGSAAALRNLMANRPAKYKD--ANIMSPGSSLPSLHV-- 754 888 AFTASHEPSDHNGIDVARGSDWSPQQQLHRWESLESQASSEDSFGLTAEEPNSSTSGA-- 945 773 LTRSIQSEMPTSSSTPKMKVSPRLNGFFSPTQKTTSSPAWSH----PDTSPIPKSSSHRT 828 887 99 609 VDGALAFLVGTLTYRSQT----NTLAIIE--SGGGIL------RNVSSLIATN 650 ------EDHRQILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWD ery Match st Local Similarity 18.6%; Pred. No. 1.6e-11; tches 540; Conservative 364; Mismatches 1038; Indels 954; Gaps 829 OPNRRÓDASDADRLIMESIMSEMPKSRIISPRLAGTOÓYLEPE-PERRSHSKNEEADRRD 1149 SAIVTPYNYQKPPFTGRNNGEMSNEKSVT----PNPKQMLV 1185 1436 SKTPPP----PPQTAQTKREVPKNKAPTAEKRESGPKQAAV 1472 946

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හි ර	RKQKALEAELDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYVF	qu	116
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ž 9	IVRVLEPGNAPONKILEGLEKIRHIDELRYP	qq	126
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ઠે	SNTYNFTKSENSNRTCSMPYAKLBYKRSSNDSINSVSGROY	ζ	171
; A	GESSEALKAEKRRIIKOKAGKKHIKEKISKLEEKKOKEKKEIKKERKELKKEEKK	qq	138
Š	GKRGOMKPSIESVSRODESKRCSVGOVDADIAHKTHSANHMODNUGELOTOTNVS	λ̈́O	177
: 유	DAKKDEKEKDTKPRVKKI,SKPDI,KPFTPSVRWIII YKZAKADRIKA	qa	143
8	T.SYSDBOLNSGROSPSONE	λö	183
· A	ARGEKELSSEPTTPPAOKGAAPPAAVSGHREIJALSSPEDITODFEETKREERGITAEORD	qa	147
8	TYPVYTEXTDDXHIKFOPHPGOORTVS DYRSBETND	λο	189
7 dd	TGLGEKPLPADATEOGHPSAAIOVTOPSGPVI.EGRHVERWKFVVP-DSPGDKG-TWRGP	q <sub>Q</sub>	152
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qq	1208	ESLGTLOFGELNLGKEERGPVMKAEDDSCHLAPVSIPEPHRATVSPSTDETPAGTLPGGS 1267
ò	1640	RUYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGG 1678
Dp	1268	FSHSALSVDRKHSPGEITGPGGHFWTSDSSLTKSPESLSSPAMEDLAVEWEGKAPG 1323
λ	1679	AQSGEFEKRDTIPIPTEGRSTDEAQGGKTSSVTIPELDDNK 1717
qq	1324	KEKEPELKSETRQQKGQILPEKVAVVEQDLIIHQKDGALDEENKPGRQQDKT-PEQKGRD 1382
δ	1718	AEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSAPNKNQLDGKKKKPTSPVK 1777
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ò	1778	PIPONTEYRTRVRANDSKANLINAERVFSDNKDSKKQNLKANSKDFNDKLPNNEDRVRGS 1837
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ò	1895	TSHTELTSNQQSANKTQAIAKQPINRGQPKPILQKQSTFPQSSKDIPDRGAATDEK 1950
Db	1525	
ò	1951	LONFAIENTPVCFSHNSSLSSLSDIDOENNN-KENEPIKETEPPDSQGEPS 2000
qu	1578	QDGAALEKTRALGLEESPAEGSKAREQEKKYWKEQDVVQGWRETSPTRGEPVGGQKEP 1635
Ś	2001	KPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQECI-SSAMPKKKKPSR 2055
Db	1636	VPAWEGKSPEGEVRYWRDRDITLQQDAYWRELSCDRKVWPPHELDGQGARFRYCEEREST 1695
ò	2056	LKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFDWKAIQEG 2107
QD	1696	FLDEGFDEQEITPLGHTPRSPWTSDFXDFQEPLPQKGLEVERWLA 1740
δ	2108	ANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPF 2159
Db	1741	
à	2160	ZSUKGPRILKPGEKSTLETKKIESESK 2186
Db	1764	PPASPPENTGORVESAPGGESPVPDTESTAPNRNEPTTPSWLAEIPPWVPKDRPLPPA 1821
λ̈́δ	2187	GIKGGKKVYKSLITGKVRSNSEISGQMKQPLQANMPSISRG 2227
qu	1822	PLSPAPAPPTPAPEPHTPVPFSWGLAEYDSVVAAVQEGAAELEGGPYSPLGKDYRKAEGE 1881
λõ	2228	RIMIHIPGVRNSSSTSPVSKKGPPLKT2263
qq	1882	REGEGGAGAPDSSSESPKVPEAGESLATRDTEQTEPEQREPTPYPDERSFQYADIYEQMM 1941
δλ	2264	GQTATTSPRGAKPSVKSELSPVARQIGQIGGSSKAPSRSGSRDSTP 2309
qq	1942	LTGLGPACPTREPPLGASGDWPPHLSTKEEAAGCNTSAEKETSSPASPQNLQSDTPAFSY 2001
Š	2310	SRPAQQPLSRPIQSPGRNSISPGRNGISPPNKLSQLPRISSPST 2353
qq	2002	ASLAGPAVPRQEPDPGPNVEPSITPPAVPPRAPISLSKDLSPPLNGSTVSCSPDRRT 2059
٥y	2354	YTSPGRQMS
qq	2060	PSPXETGRGHWDDGTNDSDLEXGAREQPEKETRSPSPHHPMFMGHSSLW 2108

677GLEISAADLAGSGSGITLPTTLEPKIEGSGKKASGGVWTEEDEGEDEDLM 726	1156 BERPTHYSIKYN 1176		1177 IDYSLKYATDIPSSQKQSFSFSKSSGQSSKTEHMSSSSENTSTPSSNAKRQNQLHPSSA 1236	787 SDGBEKLTVEKDGKEAQSSGSSATSSGKKSEATSGSSSSSAKGTGSEASGSSGASSSSG 846	1237 QSRSGQPQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSLSSLSGAEDEIG 1288	847 SGVSGESGSSVSTESGSFGTSSSGSVGSEATGSTGVDGSESGKPSKSSTEEKLP 900	Ę.	901 FTKNGEKSPISGSDITCKESSEETTSRKPIEGSDSLIEGSG-SGEWFETGSKG 952	1349 HKAVEFSSGAKSPSKSGAQTPKSPPEHYVQETPLMFSRCTSVS- 1391	953 HFESGSKVSVTSGKGPTQSGAEGSGSGPKVPKGPGAPEITTDGEESSSTSTGD 1005	1392SVQS 1407	1006 KSGGKPADKSDNKNVPKTGDKNPDITTDGEDŠTŠETŠGGBQGPKGKSKGQPPGDKGŠEVK 1065	1408 EPCSGMVSGIISPSDLPDSPGQTMPPSR 1435	1066 KPTSEVDGPGNLSGTKGKSNVPLKPTDLPEEGSGILTTSSGGKNSTFEHGTKLERLPP 1123	QAAVNAAV	1124 -KTEDKSSETPQLGLEISAGKKPEPEDGTSKEVGLEILWESTTPGSTT 1170	1493 TESTPDGFSCSSLSALSLDEPFIQKDVELRIMPPVQENDNGNE- 1536	1171 LDSDSVGLEISGSDLTKATKKPHVEIEGSGTGDEETTATTRDVSKSTKKPRVEVDGGDNG 1230	1537TBSEQPKESNENQEKEAEKTIDSEKDLLDDSDDDDIELLEECII 1580	1231 BTSGVDGKPTTPAPTPSSSAESSTSRIPTTSBASPEGGSGBAGVPESPDGSGESSTSAPD 1290	1581 SAMPTKSSRKAKKPAQTASKLPPPVARKPSQLPVYKLLPSQNRLQPQKHVSFT 1633	1291 GVSPTSSATAPEVPTTSÄSSTPDAVEESGIPSTSKPTAEPLETTÄPSTEVTSPEGSGT 1348	1634 PGDDMPRVYCVEGT-PINFSTATSLSDLTIESPPNELAAGEGVRGGAQSG 1682	1349 EESTLPPTEGSGESTTSSAPTVEPATVLPPONRNEKPEPTKDTFALPTTTTGAPQAN 1405					1729 NSAMPKGKSHKPFRVKKIMDQVQQASASSAPNKN-QLDGKKKFPTSP 1775	KKSGKV	VKPIPQNTEYRTRVRKNADSKNNLNAERVFSDNKDSKKQNLKNNSKDFNDK				:
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1893 KVTSHTELTSNQQSANKTQALAKQPINRGQPKPILQKQSTPPQSSKD 1939	
1940 IPDRGAATDEKLQNFAIENTPVCFSH-NSSLSSLSDIDQENN- 1980 	
1981 -NKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLL 2039 1867 CNKHAECIDIHPDSHFCSCPDGF-IGDGMICDDVDECNNAGMCDDDENTKC 1915	
2040 QECISSGAMPKKKKRPSRLKGDNEKHSPRNMGGILGE 2074 :	
2075 -DLTLDLKDIQRPDSEHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSD 2133 1976 TSATSSESTTAEPHVTTSISSTTSTKDMTSSKSPENVTMSSESPEVSTSSSKSTTASE 2033	
2134 SILSLKSGISLGSPFHLTPDQEEKPFTSNKGPRILKPGEKSTLETKKIESBSKG 2187 :	
2188 IKGGKKVYKSLITGKVRSNSEISGQMKQPLQANMPSISRGRTWIHIPGVRNSSSSTSPVS 2247 2079ITVKLSSKS	
2248 KKGPPLKTPASKSPSEGQTATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPS 2300	
2301 RSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGRNGISPPNKLSQL-PRTSSPST 2353 	
2354ASTKSSGSGRMSYTSPGRQMSQQNLTKQTGLSKDASSIPRSES 2396 2205 ESSTVQASETSSGTSVKSTSEPESHVTKLSITSSNPSSSVPVTSPKSTPTVPESTEQPTS 2264	
2397ASKGLNQMNNGNGANKKVELGRMSSTKSSGSESDRSERPVLVRQST 2442 ::	
2443 FIKEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQTPVLSPSLPDMSL 2493 2325 INSEEPSTTEAPTTLSPDILSTTINNLSQSSTVSTEDRSEISSENSEKPTSAPELVTSSV 2384	
2494 STHSSVQAGGWRKLPPDLLEYNDGRPAKRHDIARSHSESPSRLPINRS 2544	
2545 GTWKEEHSKHSSLPRVSTWRRTGSSSSILSASSESSEKAK-SEDEKHVNSISGTKQ 2600	
2601 SK	
2623 TNSTSQTVSSCAINGAESKTLIYQMAPAVSKTEDVWVRIEDCPINNP-RSGRSPTGN 2678 2544 KESESTTISSESSKRSQEPAGILISTVVVPTSSVSLITASEIEAITSNTPFKQGRTPITT 2603	
2679 TPPVIDSVSEKANPNIKDSKDNQAKQNVGNGSVPMRTVGLENRLNSFIQVDAPD 2732 	
2733 OKGTEIKPGGNNPVEVSETNESSIVERTPFSSSSSSKHSSPSGTVAARVIPFNYNPSPRK 2792 	······································

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RyTettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide non, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, F. anon, T.; Hickey, E.K.; Holt, I.S.; Mitte, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, F. Science 293, 498-506, 2001
A; Hickey, E.K.; Holt, I.S.; Mith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A; Reference number: A95000; MUD:21357209; PMID:11463916
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-4776
A; Residues: 1-4776
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A; Genetics:
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                                                                                                                                                                                                                                                                                         cell wall surface anchor family protein [imported] - Streptococcus pneumoniae (strain TI(C,Species: Streptococcus pneumoniae
C,Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
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CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiDates: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999
CiDates: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999
Rigitation D.O.; Bruce, D.; Mundt, M.; Doggett, N.; Munk, C.; Saunders, E.; Robinson, re, J.; White, S.; Unng, S.; Tatum, O.; Campbell, C.; Fawcett, J.; Deaven, L. submitted to the EMBL Data Library, March 1998
A;Description: Sequencing of human chromosome 16p13.3.
A;Reference number: Z14664
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolacule type: DNA
A;Residues: 1-1791 - RRIC>
A;Cross-references: EMBL:AC004493; NID:g2996648; PIDN:AAC08453.1; PID:g2996650
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A, Note: KIAA0324
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Matches	Oy 121	Qy 1255	qq	Qy 1308	109	Qy 1363	Db 160	Н	Db 207	Qy . 1474	-		Qy 1555	Db 383	Т	Db 428	.0y 1673	Db 475	Oy 1731	-		Oy 1847	Db 603	П	<del></del>		Oy 2017 Db 748	•	QY 2013 Db 807	Oy 2133

RESULT 14
T30249
cell proliferation antigen Ki-67 - mouse
Cispedies: Mus musculus (house mouse)
Cispedies: Mus musculus (house mouse)
Cispedies: Z2-oct-1399 #sequence\_revision 22-oct-1999 #text\_change 21-Jul-2000
Cispedies: T30249
Cispedies: T30249
Cispedies: T30249
A.Title: The murine Ki-67 cell proliferation antigen accumulates in the nucleolar and het A.Reference number: Z20787; MulD:96431717; PMID:8834799
A.Accession: T30249
A.Accession: T30249
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Molecule type: mRNA

147; 226 199 245 298 166 156 124 337 SAPRRL---TSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLLAMSSSQDSCISMRQSGCLPL 355 LSSVDISNFGDSI--NKSEGMPMKRRRVSFGGHLRPELFDENLPPNTP-LKRGETPTKRK 498 580 583 634 611 694 | : | : | : | STANDARK | CONTROL | : : | CLTEMPKTPVKEK QQQ----MSDTGSVLSNSANLSER QLQVTNSGDIPEPITTEILGEKV 750 797 QVQDNENAPQRCKESGELSEGSEKTSARRSSARKQKPTKDLIGSQMVTQTADYAEELLSQ 917 SVNLDEGGSAQAVHKTVTPG----KLATRNQTPVEAGDVGSPADTPEH-----SSSPQR 387 LIQLIHGNDKDSVLLGNSRGSKEARARASAALH------NIIHSQPDDKRGRREIRVL 407 HILEQIRAYCETCWEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMN 467 ELGGLQAIAELLQVDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLC-SMKGCM 526 651 ---HROILRENNCLOTLLOHLKSHSLTIVSNACGTLWNLSAR 690 731 TPVSETEPLKTASSVSKLRRSRELRHTLVETMNEKTEAVLAENTJARHLRGTFREQKVDQ 857 -----NRPAKYKDANIMSPGSSLPSLH---VRKQKALEAELDAQHLSETFDNIDNLSPK 782 ASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSSRGSLD 842 A;Cross-references: EMBL:X82786; NID:g1177527; PIDN:CAAS8026.1; PID:g1177528 A;Experimental source: strain CBA; testis C;Genetics: A;Gene: Ki-67 C;Keywords: cell cycle control; nucleus; tandem repeat : |::|:|::|: GSKNSVSQDSSGHVEQHTGRNIVEPTSGGSLLRSPGLQGAVTGNRSLLPTQSLSNSNEKE SSG-----AXRASISRSQHGIL | : | | : : | | : : | | SPRVGKIWTERWRGGMVPVQTSTETAKMKTPVRHSQQLKDEDSRV------TGRRH SONKHETGSHDAERONEGOGVGEINMAT ----SGNGQGSTTRMDHETASVLSSSSTH 499 SLGTHSPAVLKTIIK-ERPQSPGKQESPGITPPRTN-------DQRRRSGRT TPKKPTSNLHNQFTTGHANSPCTIVVGRAQIEKVSVPARPYKMLNNLMLNRKVDFSEDLS WYYAQL-QNLTKRID-----SLPLTENFSLQTDMTRRQLEYEAR-----QIRVA MEEQLG------TCQDMEKRAQRR--IARIQQIEKDILRIRQLLQSQATEAERS RALVAQLKSESEDLQQVIASVLRNLSWRADV---NSKKTLREVGSVKALMECALEVKKES ----ENKADICAVDG ALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSL----IATNED-------NP-KDQEALWDMGAVSMLKNLIHSKHKMI------AMGSAAALRNLMA-----G-----QGTIQNL-----EESWHWQNTSISEDQG---ITEKKVNIIVYATKEKHSPKTP Gaps 932; SNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSF--PRRGFV----2.9%; Score 420; DB 2; Length 2938; larity 18.6%; Pred. No. 3.3e-09; Conservative 439; Mismatches 1268; Indels 93 TLKSVLSALWN----LSAHCT--Best Local Similarity Matches 604; Conserv 80 200 338 612 751 198 157 287 388 408 584 Query Match 109 227 246 299 356 442 543 527 581 635 695 652 691 В ò Q 25 de à ठे g ò qq ò 엄 ò g 8 8 8 8 g Q Dp λ 25 8 염장

1138 1465 1478 1637 GTTAIMETPKQKLDFIGNSTGHKRRPRTPKNRAQPLEDLDGFQELFQTPAGASDPVSVEE 1696 1577 ECIIS-----AMPTKSSRKAKKPAQTA-SKLPPPVARKPSQLPVYKLLPSQNRLQPQKHV 1630 : | : :: | : : 1839 1782 RPQTPKIRAQPLEDLDGFQELFQTPAGANDSVTVEESVKMSLESSQAE--PVKTPASTKR 1839 BEQHEBEERPTNYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSKSSSGQSSKTF 1209 1636 SFTPGDDMPRVYCVEGTPI-----NFSTATSLSDLTIESPPNELAAGEGVRGGAQSGEFE 1685 ----GKRMKSLGRAPGTPAPVQEENDSTA-----FMETPKQKLDF-----TGNSSGHKR 1781 MPK-GKSHKPFRVKKIMDQVQQASASSAP------NKNQLD-----GKKKK 1771 KKV-DMKEESSALTKRIHMPGESRHNPKILKLEC--EDIKALKQSENEMLTSTVNGSKRT IGKSKKKAQPLEDLTCFQELFISPVPTNIIKKIPSKSPHTQPVRTPASTKRLSKTGLSKV 1582 ALQSPQPGHIINPASMKRQSNMSLRKDMREFSI----LEKQTQSRGRDAGTPAPMQE-EN 982 SIBSYSEDDESKFCSYGOYPADLAHKIHS-----ANHMDDND--GELDTPINYSLKY 1178 -KQKLESIENLIGLEKQSRTPKDIIGFQDSFQIPDHANG------PLVVVVKT--KKMFF 1210 HMSSSSENTSTP-----SSNAKRQNQLHPSSAQSRSGQPQKAATCKVSSINQET DSPGQTMPPSRSKTPPPPPQTAQTKREVPKNKAPTAEKRE-----SGPKQAAVNAAVQR KDRSLERER-GIGLGNYHPATENPGTSSKRGLQISTTA LPKIILRKMDV----TEBISGL--WKQSLGRVHTTQEQEDNAIKAIMEIPKETLQTAADG 1416 TRLTRQP------QTPKEKVQPLEDHSVFQE--LFQTSRYCSDPLIGNKQTRMSLRSP 1479 VQVLPDADTLLHFATESTPDGFSCSSSLSALSLDEPFIQKDVELR----IMPPVQENDN 885 AQIAKVMEEVSA----IHTSQEDRSSGSTTELHCVTDERNALRRS-----SAAHTHSNT YNFTKSEN---SNRTC----SMP---YAKLEYKRSSNDSLNSVSSSDGYGKRGQMKP 1032 SDEQLNSGRQSPSQNERWARPKHI--IEDEIKQSEQRQSRNQSTTYPVYTESTDDKHLKF QPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKPTNYSERYSE EEHLQLGEGVDTFQVSTNKVIRSSRKPAKRKLDSTAGMPNSKRMRC----SKDNTPCLE IQTYCVEDTPICFSRCSSLSSLSSAEDEIGCNQTTQEADSANTLQIAEI-KEKI-----G TRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFSSGAKSPSKSGAQTPKSP 1373 PEHYVQETPLMFSRCTSVSSLDSFESRSIASSVQSEPC-SGMVSGI-ISPSD----LP BSTPQTLDSSASRTVSKROOGAHBER--POFSGDLFHPQELFQTPASGKDPVTVDETTKI GNETESEQPKE----SNENQEKEAEKTIDSEKDLLDDSD------DDDIEILE KRDTIPTEGRSTDEAQG-----GKTSSVTIPE----LDDNKAEEGDILAECINSA SAKISLASSQAEPVRTPASTKRRSKTGLSKV--DVRQEPSTL---DLNGFQELFQMPGYANDSLTTGISTMLARSPQLGPVRTQ-843 1022 1318 1362 1524 1150 1425 1259 1631 1737 1313 8 6 8 6 8 6 Op 8 % B % 6 6 6 6 6 6 6 6 8 4 8 ò \$ A 6 6 6 6 6 8 셤 ò

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Qy 1096 QECVSPYRS	2590KHVNSISGTKQSKENQVSAKGTWRKIKENEFSPTNSTSQTVSSGATNGAESKTL 2643	දු පු
1043	2550 EHSK-HSSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDE	& g
988 494	2490 DMSLSTHSSVQAGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKR 2549	දු දු
Qy 928 AHTHSNIYN :   :   :     Db 444 SNEDSDEON	DRSERFYLDVRQSIFILARANDESASFESDAFFOSFINGERALF 	P CY
DD 395SSSRDRQ	2559 AVRKTVSTSRQTMRSRKVPEIGNNGTQVSKASIKQTLDIVAKVIGS 2604 2430 DRSRRDVIJROSTRTKRAPSDTIJRRKIJRSSASFRSIJSPSSRPASPTRSOAOTDVISPSID 2489	s a
871	RQMSQQNLTKQTGLSKNASSIPRSESASKGL : ::       ::       :	۶ و د
Oy 811 SDNFNTGNM	2315 -QPLSRPIQSPGRNSISPGRNGISPPNKLSQLPRTSSPSTASTKSSGGKM-SYTSPG 2370	Oy Dp
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C,Genetics: A,Gene: CESP:F07All.6b A,Map position: 2 A.TATFORE: 36/2: 92/2:	2225 SRGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPS-EG 2264 2392 BELTSFQEETAKKISSKSPQPEEKETLAGLKRQLKIQLINDGVKEEPTAQRKQPSRET 2449	75 25 26
A;Molecule type: DNA A;Residues: 1-2722 <wiz a:experimental="" a;cross-references:="" emb="" source:<="" td=""><td>2170 PGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQPLQANMPSI 2224 2332 PQRKITRVVRQTRNTQXEPISDNQGMEBFKESSVQKQDPSVSLTGRRNQPRTVKEKTQPL 2391</td><td>ç d</td></wiz>	2170 PGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQPLQANMPSI 2224 2332 PQRKITRVVRQTRNTQXEPISDNQGMEBFKESSVQKQDPSVSLTGRRNQPRTVKEKTQPL 2391	ç d
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യ ല്യ	2077 TLDLKDIQR-POSEHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDIL 2136	oy op
A) Reference number: Z19 A) Accession: T20532 A) Stetus: preliminary, A.Molecule trace.	2017 TPVCFSRNSSLSSLSIDSBDDLLQECISSAMPKKKPSRLKGDNEKHSPRNMGGILGEDL 2076 2178 LAKLPSSSPPLEPTDTSVTSRRQARTGLRKVHVRNELSGGIMHPQI 2223	SS GS
C;Date: 15-Oct-1999 #se C;Accession: T20532; T2 R;Palmer, S.	1983 ENEPI	장 엽
RESULT 15 T20532 hypothetical protein F0 C:Snecies: Caenorhabdit	1932 TFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSDIDQENNNK 1982 :  :	<b>상</b> 원
2919 AKT	1874 LSREKAELRKAKENKESFAKVTSHTELTSNQOSANKTQAIAKOPINRQOPKPILOKOS 1931 2010 FABN-SSGSKRRSRTSKNRSQPLEDLDGFQELFQTPAGASNPVSVEESAK 2058	දුරු
2867	1820SKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPY-CFSRNDSLSSLDFDDDDVD 1873	5 G
::     Db 2835 KKSTSRGQV	1772 PTSPVKPIPQNTEYRTRVRKAADSKANLANERVFSDNKDSKKQNLKAN 1819   :  :  :  :  :    :	S S

Db 2835 KKSTSRGQVSGRTCLRSRGTTEMPQPCEAEE 2866 OV 2763 SSSSSKHSSPSGTVAARVTPPNYNPSPRKSSADSTSARPSQIPTPVNNNTKKRD 2817	2867	Oy 2818 SKT 2820   Sp 2919 AKT 2921	RESULT 15 T20532 hypothetical protein F07A11.6b - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 C;Accession: T20532; T27777	R. Palmer, S. S. S. Bulb Data Library, October 1995 A. Reference number: Z19287 A. Accession: T20532 A. Status: preliminary; translated from GB/EMBL/DDBJ A. Wolecule type: DNA	A, Residues: 1-2722 <mil> A, Residues: 1-2722 <mil> A, Cross-references: EMBL: Z66511; PIDN: CAB54211.1; GSPDB: GN00020; CESP: F07A11.6b A, Experimental source: clone F07A11 R; Gajadety, al R; Gajadety to the EMBL Data Library, March 1996</mil></mil>	A; Reference number: 220417 A; Accession: T27777 A; Status: preliminary; translated from GB/EMBL/DDBJ	A; Residues: 1-2722 <wi2> A; Residues: 1-2722 <wi2> A; Cross-references: ENBL: 269904; PIDN: CAB54502.1; GSPDB: GN00020; CESP: F07A11.6b A; Experimental source: clone ZK20 C; Genetics: A; Gene: CESP: F07A11.6b</wi2></wi2>	A;Map position: 2 A;Introns: 36/2; 92/2; 182/2; 272/3; 344/2; 426/2; 490/1; 541/2; 700/3; 770/3; 1286/3; 1	Query Match 2.9%; Score 417.5; DB 2; Length 2722; Best Local Similarity 18.6%; Pred. No. 3.8e-09; Matches 460; Conservative 324; Mismatches 899; Indels 789; Gaps 107;	QY 811 SDNFNTGNWTVLSPYLWTTVLPSSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATENP 870	Qy 871 GTSSKRGLQISTTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCVTDERNALRRSSA 927	928 A 444 S	988 EDDESKFCSYGQYPADLAHKHSANHWDDNDCELDTPINYSLKYSDEQLN	1043 PSQNERWARPKHIIEDEIK S35 OSPGYRFIESKEIK	1096 QECVSPYRSRGANGS	QY 1140 PTNYSERYSEERQHEBEBERPTNYSIKYNBEKRHVDQPIDYSLKYATDIPSSQKQSFSFSK 1199

Page 21

QTASKLPPPVARKPSQLPVYKLLPSQNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTTT
KONLKANNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTFYCF  RSRRQSTSSTISNYTAKERKEKSGKTPLRIVPEPTGTPLLSFKHLSFKHLSFKTSTSS SRNDSLSSLDFDDDDVDLSREKAERKAKENKESEAKVTSHTELTSNQSANKTQALAKQ  SRNDSLSSLDFDDDDVDLSREKAERKAKENKESEAKVTSHTELTSNQSANKTQALAKQ  NINGSPIS

Ωp	: :  :   :   :   :   :   :   :   :   :	:   : SELENKILD 1651
οy	TSTKSGISTGS	FT 2160
QQ	1652VAAEHHEEQVQGDEDSVESSIPAPSDEPDPVTQAQEKSAHTLI	TLISDQETDQAV 1703
ò	2161SNKGPRILKPGE	2172
Ωp	1704 QSIFDEEBADEFPQYPDFGISTNEKEVSGKDPHNIKPTEPLNNGHTDLL	FSPSSSAHASE 1763
δ	2173 -KSTLETKKIESESKGIKGGKKV-YKSLITGKVRSNSEISGQMKQ	
qq	1764 KQSTKSEDDMEEDSELVVMEKEVPMEQVIAQEVHVPSEPSPWEEEVK	STSPVPKEEPIK 1823
ò	2216PLQANMPSISRGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKS	SP-SEGOTATTS 2270
g	1824 MEESPEQTPTPDLISNNESQDTPGAVNNHLHENHDAVQTPIQLQPASQHQVAQPS	PASQHQVAQPS 1878
ò	2271 PRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSI	PIQSPGRNSIS 2330
qq	1879 PRPAVAPDSQQNGPVLVSQQSQPSPM	7161 JIJNÖKMGSÖÖS
8	PS	TKOTGLSKNASS 2390
Dp	1918 SSKDINDLAAKLHKNPEALAQATRGDCSGIFQHLLLHAQGNGQNMTPEMLQLKAAFF	PEMLQLKAAFF 1974
ò	2391 IPRSESASKGLNOMNNGNGANKKVELSRMSSTKSSGSESDRSER	3R 2434
q	1975 AQQENEANÇMMQAKWKQQTINKDRIKEQERVKRMYBENBRKVEBDRREKQEKE	KORKEEERORL 2034
ò	2435 PVLVROSTFIKEAPSPTLRRKLEESSASF	ESLS 2466
q	2035 AAATAAATWAYQKAABALKQKQEVPRHGFQHVLSMYTPBARSLYEQFPGLSSYINRDSI	II SLSSYINRDSIG 2094
δλ	2467PSSRPASPTRSQAQTPVLSPSLPDMSLSTHS	SVQAGGWRKLP 2508
q	2095 ATNGVLHLPTQSIQRPSS-TASTSSNPPKAPLQPSASVNQNTIDPAE	IEEIRVQRWFYKP 2153
8	2509 PNLSPIIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKREH	EHSKHSSSLPRVSTW 2564
qq	2154 LKMSAEEAATVMAVASSDPNPPATSTVDLAAMLQQLQAAQAAQAAQQVVVTTA	SAAQQVPVVTTA 2207
ζ	2565 RRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFSP	WRKIKENEFSP 2622
q	2208 STPNPLSNLETLLSTASLANLATGGALNPLSMLALTSSLNGSSPVYQGIARVLLTMNMGQ	I . LARVLLTMNMGQ 2267
δ	VSKTEDVWVR	SGRSPTGN 2678
qa	2268 MLATHQTSELLATWN-QQETLMALLAARNGLPFAMP	-NGLPFAMPQQNQQPQMPAQGG 2315
ò	2679 TPPVIDSVSEKANPNIKDSKDNQAKQNVGNGSVPMRTVGLENRLNSFIQVDAPDQKG	FIGVDAPDQKGT 2736
qq	2316 FAIPTVLPHMSLKRNAKDQLSVGGVSDRKKSCPLHAMIGQGQQPPPPQQPMQ	эодереродемо 2367
δ	2737 BIKPGQINNPVPVSETNESSIVER	2759
qa	2368 AVAPAPPRSPSPPRKSMFENLPPEMKEKNEMFRKEILRRLDIILLEB	EELGÅEDEEDQKPDL 2427
δλ	2760 TPFSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVNNNTKKRDSK	VNNNTKKRDSK 2819
qq	2428 KQIPTSEEDTDDSKADSMGAEGSAFRRILS-RSSTWGNNSGSPSASGT	TSPS 2478
δλ		
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 25, 2004, 16:58:21; Search time 32.5 Seconds (without alignments) 4554.937 Million cell updates/sec

Title: Perfect score: 1 Sequence:

141681 seqs, 52070155 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

141681

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	reines omod Approd	P70478 rattus norv	_		drose		mus :	มนุธ ก	P78559 homo sapien	homo	gallu	rattı	homo	homo	homo sa	rattı	homo		gallı	h pe		กละก	homo	homo	homo	Q14789 homo sapien	homo	pan t	mus		caen	골	1288
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AWYH YEAST HKK MOUSE WKCR HUMAN WKCR HUMAN WKCZ HWAN WKCR MOUSE ATRX HUMAN WKCR WOUSE BRCZ ANT BRCZ ANT BRCZ RAT BSPP HUMAN ATRX PONPY
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## AL IGNMENTS

RESULT 1  APC_HUMAN STANDARD; PRT; 2843 AA.  AC P25054; Q15162; Q15163; DT 01-MAX-1992 (Rel. 22, Created)  DT 01-MAX-1992 (Rel. 23, Last sequence update)  DT 15-MAR-2004 (Rel. 43, Last annotation update)  DE Adenomatous polyposis coli protein (APC protein).  GN APC OR PP2.5.  Human).	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chrimates; Catarrhini; Hominidae; Homo.  NCBI TAXID=5606;  (1] SEQUENCE FROM N.A.  MEDLINE=91335210; PubMed=1651562;  Kinzler K.W., Nilbert M.C., Su LK., Vogelstein B., Bryan T.M., Itury D.B., Smith K.J., Preisinger A.C., Hedge P., McKechnie D., Finniear R., Markham A., Groffen J., Boguski M.S., Alteschul S.F., Horil A., Ando H., Miyoshi Y., Miki Y., Nishisho I., Nakamura Y.; "Identification of FAP locus genes from chromosome 5q21."; Science 253:661-665(1991).	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. TISSUE=Fetal brain; MEDLINE=91330307; PubMed=1678319; JOSIYN G., Carlson M., Thliveris A., Albertsen H., Gelbert L., Samowitz W., Groden J., Stevens J., Spirio L., Robertson M., Sargeant L., Krapcho K., Wolff E., Burt R., Hughes J.P., Warrington J., McPherson J.D., Wammuth J., Le Paslier D., Abderrahim H., Cohen D., Leppert M., White R.; "Identification of deletion mutations and three new genes at the familial polyposis locus."; [3] ASSOCIATION WITH CATENINS. [3] ASSOCIATION WITH CATENINS. Su LK., Vogelstein B., Kinzler K.W.; "Association of the APC tunor suppressor protein with catenins."; [4] Science 262:1734-1737(1993).	DISEASE.  WEDLINE=95174843; PubMed=7661930; Hamilton S.R., Liu B., Parsons R.E., Papadopoulos N., Jen J., Powell S.M., Krush A.J., Berk T., Cohen Z., Tetu B., Burger P.C., Powell S.M., Taqi F., Booker S.V., Petersen G.M., Offerhaus G.J.A., Tersmette A.C., Giardiello P.M., Vogelstein B., Kinzler K.W.; The molecular basis of Turcot's syndrome."; New Engl. J. Med. 332:839-847(1995). New Engl. J. Med. 332:839-847(1995).  MEDLINE=97094176; PubMed=8940264; Escles D.M., van der Luijt R.B., Breukel C., Bullman H., Bunyan D., Fisher A., Barber J., du Boulay C., Primrose J., Burn J., Fodde R.; "Hereditary desmoid disease due to a frameshift mutation at codon 1924 of the APC gene.";
RES APC AC DT DT DT DT OS	OOC OCC OCC OCC OCC OCC OCC OCC OCC OCC	RAPAK RAPAK	RAY RAY RAY RAY RAY RAY RAY RAY RAY RAY

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Saba S., Nakamura Y.;
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 MEDITAL S135211; PubMed=1651563; Nishisho I., Nakamura Y., Miyoshi Y., Miki Y., Ando H., Horii A., Koyama K., Utsunomiya J., Baba S., Hedge P., Markham A., Krush A.J., Petersen G.M., Hamilton S.R., Nilbert M.C., Levy D.B., Bryan T.M., Preisinger A.C., Smith K.J., Su L.-K., Kinzler K.W., Vogelstein B., "Mutations of chromosome 5q21 genes in FAP and colorectal cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakatsuru S., Yanagisawa A., Ichii S., Tahara E., Kato Y.,
Nakamura Y., Horii A.,
"Somatic mutation of the APC gene in gastric cancer: frequent
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TISSUE-Peripheral blood;

TISSUE-Peripheral blood;

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WEDLINE=98400248; PubMed=9731522;
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STRAIN=Sprague-Dawley, and Fischer 344/N;
MEDLINE=95148647; PubMed=7846077;
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InterPro; IPR008938; ARM.
InterPro; IPR000255; Armadillo.
Pfam; PF00514; Armadillo.seg; 4.
SNART; SWO0185; ARM; 5.
PROSITE; PS50176; ARM; REPEAT; 1.
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STRAIN=FIGEDER 344/N; TISSUE=Brain;
MEDIJNB=96116966; PubMed=8563176;
TOYOTA M., Ushijima T., Kakiuchi H., Watanabe M., Imai K., Yachi A., Sugimura T., Nadao M.;
Sugimura T., Nadao M.;
MINING CINING Of the rat APC gene and assignment to chromosome 18.";
Mamm. Genome 6:746-748(1995).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Figure 1. Matanabe M., Value T., Toyota M., Imai K.,
Kakiuchi H., Watanabe M., Vabhijima T., Toyota M., Imai K.,
Weisburger J.H., Sugimura T., Nagao M.;
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Weisburger J.H., Sugimura T., Nagao M.;
Weisburger J.H., Sugimura T., Nagao M.;
Fyrot. Natl. Sugimura T., Nagao M.;
Proc. Natl. Acad. Sci. U.S.A. 92:910-914(1995)
-!- FUNCTION: Tumor suppressor. Promotes rapid degradation of CTNNB1
and participates in Mrt signaling. APC activity is correlated with
its phosphorylation state (By similarity)
-!- SUBUNT: Forms homooligomers. Associates with catenins. Binds
axin (By similarity).
-!- PTM: Phosphorylated by GSK3B (By similarity).
-!- PTM: Phosphorylated by GSK3B (By similarity).
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Wht signaling pathway; Anti-onco
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EMBL, U02937, AAA03443.1; -.
PIR, I49505, I49505.
HSSP, Q02248; 3BCT.
axin (By similarity).
ALTERNATIVE PRODUCTS:
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"APC gene messenger KhA: novel isoforms that lack exon 7.";

"APC gene messenger KhA: novel isoforms that lack exon 7.";

Cancer Res 53.5589-5591 (1933).

-!- FUNCTION: Tumor suppressor. Promotes rapid degradation of CTINNB1 and participates in Wnt signaling. APC activity is correlated with its phosphorylation state (By similarity).
-!- SUBUNIT: Forms homooligomers. Associates with catenins. Binds
                                                                                                                                                                                                                                                                                                                                                                                                      2756 AERTPPSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVGSSTKKR
                                                                                                  2457 EESASFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIE
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                                                                             2517 YNDGRPAKRHDIARSHSBSPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS.
STRAIN=C57BL/6J, and CAST/EI; TISSUB=Brain;
BELLINES-22631011, PubMed=1150108.
Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R. Luongo C., Gould K.A., Dove W.F.;
Multiple intestinal neoplasia caused by a mutation in the murine homolog of the APC gene.";
Science 256:668-670(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R. Luongo C., Gould K.A., Dove W.F.; Science 256:1114-1114(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEAIN-BALB/c; TISSUB-Liver;
Dicker F., Lambertz S., Reitmair A., Ballhausen W.G.;
"The murine APC gene: alternative splicing of 5' untranslated
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Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                DSKTDSTESSGTQSPKRHSGSYLVTSV 2843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSKTDSTESSGAQSPKRHSGSYLVTSV 2842
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MEDLINE=94061824; PubMed=8242607;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                  Isold=061315-4; Sequence=VSP 004116, VSP 004117;
-:- TISSUB SPECIFICITY: Expressed in liver, spleen, kidney, heart, lung, brain, ercmach, intestine, testis and ovary.
-:- PTM: Phosphorylated by GSK3B (By similarity).
-:- SIMILARITY: Contains 7 ARM repeats.
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GO; GO:0005737; C:Cytoplasm; IDA.
GO; GO:0005634; C:Cytoplasm; IDA.
GO; GO:0006634; C:Cytoplasm; IDA.
GO; GO:0006634; P:Deta-catenin binding; IDA.
GO; GO:0008952; P:anterior/posterior pattern formation; IMP.
GO; GO:00099952; P:axis specification; IMP.
GO; GO:0009993; P:dorsal/ventral pattern formation; IMP.
GO; GO:0016055; P:Wint receptor signaling pathway; IDA.
InterPro; IPR000225; Armadillo.
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COLLED COIL (POTENTIAL)
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ASP/GLU-RICH (ACIDIC)
HIGHLY CHARGED.
Event=Alternative splicing; Named isoforms=4;
                                                                                              Sequence=VSP_004116;
                                                                                                                                              IsoId=Q61315-3; Sequence=VSP_004117;
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                                                IsoId=Q61315-1; Sequence=Displayed;
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ARM 1.
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DB 1; Length 2845;

### LOCAL SAMILALITY 90.78*, Pred. No. 0;  ### RANAS TO CLASSE VALIDATIONS NAME THAT THE PASS NAME TO THE PA	1019	OY 1081 STDDKHLKPQPHFGQQECVSPYRSRGANGSEINRVGSNHGINQNVSQSLCQEDDYEDDKP 1140 1079 NIDDKHLKPQPHFGQQECVSPYRSRGISGSEINRMGSSHAINQNVNQSLCQEDDXEDDKP 1138	QY 1141 TNYSERYSEEGGH-EEBERPTNYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSK 1199	OY 1200 SSSGQSSKTEHMSSSSENTSTPSSNAKRONOLHPSSAGSRSGDPOKAATCKVSSINOETI 1259	QY         1260 QTYCVEDTPICFSRCSSLSSAEDEIGCNOTTQEADSANTLOIAEIKEKIGTRSAEDP 1319           Db         1258 QTYCVEDTPICFSRCSSLSSAEDSEIGCDQTTQEADSANTLQTAEVKENDVTRSAEDP 1317	QY 1320 VSEVPAVSQHPRTKSSRLQGSSLSSESARH-KAVEFSSGAKSPSKSGAÇTPKSPEHYVQ 1378 :	QY 1379 ETPLMFSRCTSVSSLDSFESRSIASSVQSEPCSGWVSGIISPSDLPDSPGQTWPPSRSKT 1438	QY 1439 PPPPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPD 1498 DD 1438 PPPPPQTVQAKREVPKSKVPAAEKRESGPKQTAVNAAVQRVUPDVDTLLHFATESTPD 1497	QY         1499         GFSCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTID         1558           DD         1498         GFSCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPEESNENQDKEVEKP-D         1556	QY 1559 SEKOLLDDSDDDDIEILEECIISAMPTKSSRKAKKPAQTASKIPPVARKPSQLPVYKLL 1618  Db 1557 SEKOLLDDSDDDDIEILEECIISAMPTKSSRRAKKLAQTASKLPPPVARKPSQLPVYKLL 1616	OY 1619 PSONRLOPOXHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGG 1678  1617 PAQNRLQAQXHVSFTPGDDVPRVYCVEGTPINFSTATSLSDLTIESPPNELATGDGVRAG 1676	OY 1679 AQSGEFEKRDIIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDIIAECINSAMPKGKSH 1738	QY 1739 KPFRVKKIMDQVQQASASSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNN 1798 Db 1737 KPFRVKKIMDQVQQASSTSSGANKNQVDTKKKKRTSPVKPMPQNTEYRTRVRKNTDSKVN 1796	QY 1799 INAERVFSDNKDSKKQNLKANSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSR 1858 1997 VNTEETFSDNKDSKKPSLQTNAKAFNEKLPNNEDRVRGTFALDSPHHYTPIEGTPYCFSR 1856	QY 1859 NDSLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQPI 1918	OY 1919 NRGOPKPILOKOSTFPOSSKDIPDRGAATDEKLONFAIENTEVCFSHNSSLSSLSDIDOE 1978  1917 NRAQSKPVLOKQPTFPQSSKDGPDRGAATDEKLONLAIENTPVCFSRNSSLSSLSDIDOE 1976	QY 1979 -NNNKENEPIKETEPPDSQEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSISIDSEDD 2037	QY 2038 ILQECISSAMPKKKRERILKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSE 2097	QY 2098 NFDWKALQEGANSIVSSLHQ-AAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEE 2156
ed. No. 0,  Mismatches 155; Indels 12; Gaps  120ELEDNSNHLTKLETEASNMKEVLKOLOGSIEDEAM  LROELEDNSNHLTKLETEASNMKEVLKOLOGSIEDEAM  LROELEDNSNHLTKLETEASNMKEVLKOLOGSIEDETM  LROELEDNSNHLTKLETEASNMKEVLKOLOGSIEDETM  PGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR  PGILIALDLDKEEKEKDWYYAGLONLTKRIDSLPLTENFSL  LLLADLDKEEKEKDWYYAGLONLTKRIDSLPLTENFSL  LLLADLDKEEKEKEDWYYAGLONLTKRIDSLPLTENFSL  GLGTCODMEKRAORRIARIOOIEKDILRYGOLOSOAA  GGCTCODMEKRAORRIARIOOIEKDILRYGOLOSOAA  GGCTCODMEKRAORRIARIOOIEKDILIOOLOSOAA  GGCTCODMEKRAORRIARIOOIEKDILROOIEKDILIOOLOSOAA  GGCTCODMEKRAORRIARIOOIEKDILIOOLOSOAA  GGCTCODMEKRAORRIARIOOIEKDILOOLOSOAA  GGCTCODMEKRAORRIARIOOIEKDILOOLOSOAA  GGCTCODMEKRAORRIARIOOIEKDILIOOLOSOAA  GGCTCODMEKRAORRIARIOOIEKDILIOOLOSOAA  GGCTCODMEKRAORRIARIOOIEKDILIOOLOSOAA  GGCTCODMEKRAORRIARIOONOTOROA  MNEGOSSLESILVYRKOKALEABLDAOHILSKYMEEVSAIHTS  MNEHDDRR SDNENTGRANTVLSPYLMTTVLESSSSEGG  MNEHDDRR SDNENTGRANTVLSPYLMTTVLESSSSEGG  MNEHDDRR SDNENTGRANTVLSPYLMTTVLESSSSEGG  MNEHDDRR SDNENTGRANTVLSPYLMTTVLESSSSEGG  MNEHDDRR SDNENTGRANTVLSPYLMTTVLESSSSEGG  MNEHDDRR SDNENTGRANTVLSPYLMTTVLESSSSEGG  MNEHDDRR SDNENTGRANTVLSPYLMTTVLESSSSEGG  MNEHDDRR SDNENTGRANTVLSPYLMTTVLESSSSEGG  MNEHDDRR SDNENTGRANTGRANTCSMPYRALETSNAGTILOON  THE HILL HILL HILL HILL HILL HILL HILL HI	—	ў Э				<u></u>						о р	———			<u> </u>	<b>υ</b> Δ	<b>υ</b> Δ	<u></u>
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01-FEE-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
Microcubule-associated protein 1A (MAP 1A) (Contains: MAP1 light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BESASFESLSPSSRPDSPTRSQAQTPVLSPSLDPMSLSTHPSVQAGGWRKLPPNLSPTIE
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                                   KPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQP
                                                                                                                                                                                                            ASKGLNOMNGNGANKKVELSRMSSTKSSGSESDRSERPVLVROSTFIKEAPSPTLRRKL
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                                                                         KPFTSNKGPRILKPGEKSTLEAKKIESENKGIKGGKKVYKSLITGKIRSNSEISSQMKQP
                                                                                                                                                                     LOANMPSISRGRIMIHIPGVRNSSSTSPVSKKGPPLKTPASKSPSEGQTATTSPRGAKP
                                                                                                                                                                                                                                                                                                SVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGRNGI
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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J. Biol. Chem. 267:16561-16566(1992).
-!- FUNCTION: Structural protein involved in the filamentous cross-
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Brading=Brain;
Langkopf A., Hammarback J.A., Mueller R., Vallee R.B., Garner C.C.
Imigropf A., Hammarback J.A., Mueller R., Vallee R.B., Garner C.C.
"Microtubule-associated proteins 1A and LC2. Two proteins encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKRDSKTDSTESSGTQSPKRHSGSYLVTSV 2843
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bridging between microtubules and other skeletal elements.
SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate with MAPIA and MAPIB proteins.
TISSUE SPECIFICITY: BRAIN, HEART AND MUSCLE.
DEVELOPMENTAL STRGE: EXPRESSED LATE DURING NEURONAL DEVELOPMENT APPEARING WHEN AXONS AND DENDRITES BEGIN TO SOLIDIFY AND STABILIZE
                                                                                                                                                                  THEIR MORPHOLOGY.

-1- DOWALN: THE basic region containing the repeats may be responsible for the binding of MAPIA to microtubules.
-1- PTM: Ucz is corrected may be phosphorylated by cAMP kinase.
-1- PTM: LC2 IS CORRERESSED WITH MAPIA. IT IS A POLYBEPTIDE GENERATED FROM MAPIA BY PROTECLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH BOTH MAPIA AND MAPIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 IGADNLPGINGLLQRK-----VAELEEEQSQGSSSYSDWVKNLISPELGVVFFNVPD
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AA REPEATS OF K-K-[DE]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylation.

Hosphorylation.

MAP1 LIGHT CHAIN LC2.

LXS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.3%; Score 476; DB 1; L. L. 18.5%; Pred. No. 3.2e-10; Conservative 364; Mismatches 1038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    609 VDGALAFLVGTLTYRSQT----NTLAIIE--SGGGIL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S
or send an email to license@isb-sib.ch).
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CHAIN ?2465 277
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2774 AA;
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us-09-442-489f-7.rsp

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QY         1718 AEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSAPNKNQLDGKKKKPTSPVK 1777           :	1474APBHSIPEPTQTDRAPDRKGTDDKEGKEEASBEKEQVLEQKDWALGKEGET 1895 TSHTELTSNQQSANKTQAIAKQPINRGQPKPILQKQSTFPQSSKDIPDRGAATDEK 1525LDQEARTAEQKDETLKEDKTQGQKSSFVEDKTTTSKETVLDQKSAEXADSVEQ	OY 1951 LQNFAIENTPVCFSHNSSLSSLSDIDQENNN-KENEPIKETEPPDSQGEPS 2000	DD 1636 VPAWEGKSPEQEVRYWRDHDITLQQDAYWRELSCORKVWFPHELDGGGARPRYCEEREST 1695  QY 2056 LKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFDWKALQEG 2107  DD 1696 FLDEGPDEQEITPLQHTPRSPWTSDFKDFQEPLPQKGLEVERWLA 1740	Qy 2108 ANSIVSSLHQAAAAACLSRQASSDSDILSLKSGISLGSPPHLTPDQBEKPF 2159  Db 1741	2160TSNKGPRILK   :   1764 PPASPPEMTGORVPSA	Qy 2187GIKGGKKVYKSLITGKVRSNSEISGQMKQPLQANMPSISRG 2227	Qy 2228 RTMIHIPGVRNSSSTSPVSKKGPPLKTPASKSPSE2263	QY 2264GQTATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTP 2309	QY 2310SRPAQOPLSRPIQSPGRNSISPGRNGISPPNKLSQLPRISSPST 2353	QY 2354 ASTKSSGSCKMSYTSPGRQMSQONLTKQTGLSKVASSIPRSESASKGLNQMNNGNGA 2410	QY 2411 NKKVELSRMSSTKSSGSBD 2430    :	QY 2431 RSBRPVLVRQSTFIKEAPSPTLRRKLEESASFESLSPSSRPASPT 2475	QY 2476 RSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDGRP 2522	QY 2523 AKRHDIARSHSESPSRLPINRSGTWKREHSKHSS6LPRV9TWRRTGSSS 2571 :   :   :	Qy 2572 SILSASSESSEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFSPTN- 2624
932 SNTYNFTKSENSNRTCSMPYAKLEYKRSSNDSLNSVSSSDGY :	OY 1029 LKYSDEQLNSGROSPSQNERWARPKHILEDEIKQSEGROSRNQST 1073  DD 492 ARGEKELSEPTYPPAGKGAAPPAAVSGHRELALSSPEDLTQDFELKKERGLLAEQRD 551  OY 1074 TYPVYTESTDDFALKFQPHFGGCSPSTSSRGANGSFUR- 1114  DD 552 TGLGEKPLPADATEQCHPSAAIQVTQPSGPVLEGEHVEREKEVVP-DSPGDKGS-TNR- 609	QY 1115VGSNHGINQNVSQSLCQEDDYEDDKPTNYSERYSEEQ 1152  Db 610 DSGAEVEKETWEERKQREAELGPENTAAREESBAEVKEDVIEKAELEEMEETHPSDEE 669  QY 1153 HEBERRPTNYSIKYNEEKRHVDOPIDYSLKYATDIPSSOKOSFSFSKSSG 1203	670 GESTKAESFYQKHTQEALKASPKSREALGGRDLGFQGKAPEKETASFLSTLAT  1204 QSSKTEHMSSSSENTSTPSSNAKRQNQLHPSSAQSRSGQPQ  121	KAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSLSSAEDEIGCNGTTQEADSANTLQI	SARHKAVEFSSGA  :  :  :  SSRTEATQGLDYVPSAGT	OY 1359 KSPSKSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFESRSIASS 1404	VOSEPCGGWVSGIISPSDLPDSPGQTMPPSRSKTPPP 		1471AVNAAVQRQVLPDADTLLHFATESTPDGFSCSSSLSA  1671AVNAAVQROQVLPDADTLLHFATESTPDGFSCSSSLSA	1509 LSLDEPFICKDVELRIMPPYQENDNGNETESEQP  1104 GTLPGEVRISTEEATEPQKOEVLRFTDQSLSPEDAESLSVLSVVSVVENDTKOEATPRSE	SRKAKK	1594 PAQTASKLPPPVARKPSQLPVYKLBSQNRLQPQKHVSFTPGDDMP		1679 AQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNK	Db 1324 KEKEPELKSFTRQQKGQILPEKVAVVBQDLIIHQKDGALDEENKPGRQQDKT-PEQKGRD 1382

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MEDLINE=20196006; PubMed=10731132;
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2749 SETNESSIVERIPPS-----SSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTS---
                                                                                                                                                                                               2559 GLSSESGRVERLREKGRPGRRAPGRAKPASPARRLDIR----GKRSPTPGKGPVDRTSRTV
                                   ---APAVSKTEDVWV
                                                         2382 LSSEQPLRPGKSSGGPPCSLSSEVEAGPQGCATDPRPHCGELSPSFLNPPLPPSTDDSDL
                                                                               2660 RIEDCPI----NNPRSGR-SPTGNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNGSVPMR
                                                                                                     2442 STEEARLAGKGGRRRVGRPGATGGPCPMAD---ETPPTSASDSGSSOSDVPPETEECP
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 3 AND 4), FUNCTION, ALTERNATIVE PROMOTER USAGE, TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, AND MUTANTS E9 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rebay I., Chen F., Heiso F., Kolddziej P.A., Kuang B.H., Laverty T., Suh C., Voas M., Williams A., Rubin G.M.;
"A genetic screen for novel components of the Ras/mitogen-activated protein kinase signaling pathway that interact with the yan gene of Drosophila identifies split ends, a new RNA recognition motif-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20025936; PubMed=10556062;
Wiellette E.L., Harding K.W., Mace K.A., Ronshaugen M.R., Wang F.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "spen encodes an RNP motif protein that interacts with Hox pathways to repress the development of head-like sclerites in the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20171275; PubMed=10704397;
Klang B.H., Wu S.C.-Y., Shin Y.-A., Luo L., Kolodziej P.A.;
"split ends encodes large nuclear proteins that regulate neuronal
cell fate and axon extension in the Drosophila embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1), SUBCELLULAR LOCATION, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                              2715 TVGLENRLNS----FIQVD-APDQKGT-EIKPGQNNPV-------
                                                                                                                                                                                                                                                                                                    SPEN_DROME STANDARD; PRT; 5560 AA. Q8SX83; Q9WEL1; Q9WFL2; L10-OCT-2003 (Rel. 42, Tested) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND TISSUE SPECIFICITY. STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Embryo;
MEDLINE=20157049; PubMed=10655223;
                                   -STSQTVSSGATNGAESKTLIYQM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Development 126:5373-5385(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 4).
                                                                                                                                                                                                                       2800 ARPSQIPTPVNNNTKK 2815
                                                                                                                                                                                                                                             2616 PRPRSTPSQVTSAEEK 2631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics 154:695-712(2000)
                                                                                                                                                                                                                                                                                                                                                              Split ends protein.
SPEN OR CG18497.
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TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Embryo;
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SPEN_DROME
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2216 KNSSSHISRPHGCGGSSASSSKHHRRDKHQKGSASSIETNSSIEVVVDPISQTKHNLN 2275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2276 TSEEELQSHQPKREKER-----EHFSSHANSSSSRHKSKRDHHHHREK--KRHSVAES 2326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2364 -----SGKLHHQHHRRSVERKSSR---GS-----DEGHHSSSKSLRAKLMMLSS 2404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 AMASSGQIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 QNEGQGVGEINMATSGNGQGSTTRMDHETASVLSSSSTHSAPRRLTSHLGTKVEM---VY 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 PRRGFVNGSRESTGYLEE----------LEKERSLLLADLDKEEK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 -----AQRRIARIQQIEKD----ILRIRQLLQSQATEAERSSQNKH-ETGSHDAER 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 TCWEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAEL 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2156 NHSAGGGGSCGGSSHQIHHEDYVKRIRMENSQNISVHSSNQRLNDRRDSKEHKSSSFKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1846 SSSSSKXI-----SSTHD--KLHSKHNNRSESDKKIKKSDKNASSSDKRKNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 EKDWYYAQLQNLTKRIDSLPLTENFSLQTDMTRRQLEYEARQIRVAMEEQLGTCQDMEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1997 DKEQKEKEIREKDLREKEGRERDNREKELRDKDLREKEMREKEGREKELHREKDQREREH
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                                                                                                                                                                                                                                                                                                                                                                                          2 AAASYDQLLKQVE---ALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDE
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                                                                                                                                                                                                                                                          Query Match
3.3%; Score 474; DB 1; Length 5560;
Best Local Similarity 18.5%; Pred. No. 8.3e-10;
Matches 621; Conservative 479; Mismatches 1219; Indels 1034;
                                 Transcription regulation, Repressor; Developmental protein; Nuclear protein; Repeat; RNA-binding; Coiled coil; Alternative promoter usage; Alternative splicing. DOMAIN 554 632 RNA-BINDING (RRM) 1. DOMAIN 656 730 RNA-BINDING (RRM) 2. DOMAIN 734 806 RNA-BINDING (RRM) 3.
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             PROSITE; PS50917; SPOC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=5; Synonyme=Speni; Internative Epideing of isoform 1; Note=Produced by alternative Epideing of isoform 2; Note=Produced by alternative Epideing of isoform 2; Note=Produced by alternative Epideing of isoform 2; In Stage Specificity: Ubjecticus. Expressed prior to callularization in stage 3 embryos, and in blastoderm cells, including pole cells. Expressed throughout the rest of embryogenesis. Later, it is expressed at higher level in epidermal cells and CNS.

DEVELOPMENTAL STAGE: Isoform 3 is expressed both maternally and
                                                                                                                                                                                                                                                                                                            Development 130:3125-3135 (2003).

-!- FUNCTION: Probable corepressor protein, which regulates different key pathways such as the EGF receptor and Wg pathways. Involved in neuronal call fate, survival and axon guidance, cell cycle regulation and repression of head identity in the embryonic trunk. May act with the Hox gene Deformed and the EGF receptor signaling pathway. Positive regulator of the Wg pathway in larval tissues but not in embryonic tsues. May act as a transcriptional corepressor protein, which repress transcription via the recruitment of large complexes containing histone deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ğ
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--- SIMILARITY: Belongs to the Spen family.
--- SIMILARITY: Contains 3 RNA recognition motif (RRM) domains.
--- SIMILARITY: Contains 1 SPOC domain.
--- CAUTION: It is uncertain whether Met-1 or Met-7 is the initiator.
                                        EGF receptor pathway,
                                                                                                                                                        FUNCTION ON WG PATHWAY.
MEDLINE=22668876; PubMed=12783785;
Lin H.V., Doroquez D.B., Cho S., Chen F., Rebay I., Cadigan K.M., "Splits ends is a tissue/promoter specific regulator of Wingless
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     008566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins.
SUBCELULAR LOCATION: Nuclear.
ALTENATIVE PRODUCTS:
Comment=2 isoforms, 1 (shown here) and 2, are I alternative promoters,
Event-Alternative splicing; Named isoforms=4;
Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note=No experimental confirmation available;
Chen F., Rebay I.;
"split ends, a new component of the Drosophila E regulates development of midline glial cells.";
curr. Biol. 10:943-946(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q8SX83-2; Sequence=VSP_008565, VSP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0007411; P:axon guidance; IMP.
GO; GO:0008347; P:glia cell migration; IMP
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q8SX83-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfem; PF00076; rrm; 3. _____
SMARY; SM00360; RRM; 3.
PROSITE; PS50102; RRM; 3.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF221715; AAF34661.1; ALT_INIT.
EMBL; AE003590; AAF51534.2; -.
EMBL; AE003590; AAF51535.2; -.
EMBL; AE003590; AAN10511.1; -.
EMBL; AY094788; AAN1141.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF188205; AAF13218.1; -.
EMBL; AF184612; AAF26299.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0016977; spen
                                                                                                                                                                                                                                                                                        signaling.";
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537

----K 792

Db 3503 PPSPVKIEPPTISKLQQPL	Oy 1668 BLAAGEGVRGGAQSG	1713	3618	Qy 1771 KPTSPVKPIPQNTEYRT	OY 1817 KONSKDENDKLPNNED	3728	QY 1852 TPYCFSRNDSLSSLPFDDDVUL	1909	3833 MQFWHQQMIQRQQHMQQQQ	Qy 1969 LSSLSDIDQENNNKENEPIKE	2027	3917	Qy 2087 DSEHGLSPDSENFDWKAIQEGAN	3962	Qy 2147 PFHLTPDQEEKPFTSNKGPRILK	7022	4041	2267	Db 4075TPLNVIQNTPKIIVQQHIVA		QY 2378 LTKQTGLSKNASSIPRSESASKG	4168	2438	Db 4220EMQAIAPAFIFNPQPGNQSMA	4278 TVGRPPGRG	QY 2512 SPIIEYNDGRPAKRHDIARSHSE	4338	Qy 2572 SILSASSESSEKAKSEDEKHVNS  A 2572 SILSASSESSEKAKSEDEKHVN	4391 SVLTAA
: : :     :		2569 HSHFGKRNSNSTRIASDSESQSQPAPDLTIKQEHPIAPAQEIKREQLSDEEQKFKSR 2625	842 -DSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQIS 881	TTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCVTDERNALRRSSAAHT	ADTSAAQTPLVMTPLTPSIFDVHSSSECKTKFDNFDDLKTECSSIPLEISAGER	951 HSMITNFIRSENSKITCSMFYAKLESKRÖSNUSLANGVSSSUGIGKKOMFEDISTSBUU 990 2740RKHKERKEKKREKLRNMTEATVPNSPTTNDISSEKLSKEERHRLKKSKKKKKSKSMDN 2794	991 ESKFCSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNSG 1039	SCNTKIYNSGAHPSTSPSLPATPTSAPSTAQTSKRGEDKMFFIFGI-ISDEESS	1040 RQSPSQNERWARPKHIIEDEIKQSEQRQSTATYPYYTESTUDKHIKTQFHFG 1094 2849 -OPPGABETUNDDIIPSSVSTTGPIVŠAALOTYKOEPSTPNSKNEEHIOLIVHEP 2902	QQECVSPYRERGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKPTNYSERYSEEEQHE	2903 EQQ-QQLERSRLSGGSSSSSHADRERHRREKREKKRREXSQREQQNQIHQ 2951	EEERYINYSIKYNEEKRHVDQPIDYSLKYATDI	KSSKVETKVDDDNSVDMDEAGRALEAQLMSDPDTKPISEEATPSTAATYRSDMTDVFRPS	1188 PSSQKQSFSFSKSSSGQSSKTEHMSSSSENTSTPSSNAKRQNQLHPSSAQSRSGQPQKAA 1247 3012 DNEDNNSYDMTKQGVKSEQDSQHKSKDKKKKKRRKRKRKRKRGKEKDRSKGPRLQQQRRSKINAS 3068		3069 TSSAPPTPGKLTVNVQAASKHADLQLDAKHISSPPVC-KPSPSLPCLIGDDDD 3120	1294 QEADSANTLQIAEIKEKIGTRSAEDPVSEVP-AVSQHPRTKSSRLQGSSLSSESA 1347 121	RHKAVEPSSGAKSPSKSGAQTPKSPPEHYVOSTPLMFSRCTSVSS	CKKKESFIPGFDGQ	LDSFBSRSIASSVQSFPCSGMVSGIISPSDLPDSPGQTWPPSRSKTPPPPPQTAQTKREV	3229 LDDRISESAVQSISAE-FNSTSLLDNIADERKIP-VASFFRAIKFLUKLESSKSKV 3282 1453 DKNKADTBEVDEGEDRODAINMAAVODVOVIDDADTII.HPATESTDNGESCRSGISA 1508	FIGURE 1 STATES OF STATES	LSPVQENDNGNETS			VLDPEEINKAVQSLKHEDMMDIKADTPQSEROLQIDTDTEENPDEADSSGPSLKIDETVQ	1580 ISANETKS-SKRAKKEACTOOF 151/  S                               3582 ISANESTED SERVITKLEFELD TEKTVEAGE 3443 SSSSEKSISNNSPTPRETANIDIENVESOPKLSNESTED SEVITKLEFELD TEKTVEAGE 3502	1618 LPSQNRLOPQKHVSFTPGDDMPRVYCVEGT-PINFSTATELSDLTIESPPN 1667	
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ONAMPQASTPKQGPITPQ-QAIRTQSLIMQPPTISIPE 3617 3996 AQNQVPPPQTQ--GNAIHYPQNQG-KDSTP----- 4120 NSISGTKOSKENOVSAK-GTWRKIKE-NEFSPTNSTSOT 2629 : : | : : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : 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| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : LVQPVQTVLPAPHSTGSGISANSVINLDLSNVISSCSN 3558 GEFEKRDTIPTEGRSTDEAGGGKTSS-----VTIPE 1712 GKSHKPFRVKKIMDQVQQAŞASŞ--SAPNKNQLDGKKK 1770 TRVRK---NADSKNNLN----AERVFSDNKDSKKONL 1816 ------RVRGSFAFDSPHHYT-----PIEG 1851 VQTTPQLMTIPLQKMTPIQVPHPPTIISKVVTVQPQQA 3787 LSREKAELRKAKENKESE---AKVŢSHŢELŢSNQQSAN 1908 STFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSS 1968 QLHGQSQQ----CHTSAP---QHQMH 3869 ETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSS 2026 14QQHP-----TQKQHQAQQQFWQQ----1QQHQS 3916 WKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRP 2086 | ::| | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : 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KGLNOMNNGNGANKKVELSRMSSTKSSGSESDRSERPVL 2437 ASFESTSPSSRPAS----PTRSQAQTPVLSPSLPDMS 2492 KVGGFPLNSVTAAPPGVDSLVVQPGDNGVQTRLRKPVT 4337 ESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSS 2571 LOQQQQLDIQRKGMEMVTSATSTPLPTPI-----PTS 4390 TSIF------ASQOHNSQL------

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2630 VSSGATNGAESKTLIYQMAPAVSKTEDVWVRIEDC--PINNPRSGRSPT-GNTPPVIDSV 2686
                                                                   4440 ISSVAPSAEDQRP---RLILTINKTQPSIKNİSEMEQTİQQQQQQQSEVISNTDPIGGDN 4496
                                                                                                                                          2687 SEKANPNIKDSKDNQAKON------VGNGSVPMRTVGLENRLNSFIQVDAPD-QK 2734
                                                                                                                                                                                                                                                                                             2735 GTEIKP---GON------NPV------PVSETNESSIVERTPFSSSSSK 2769
                                                                                                                                                                                                                                                                                                                                                                     4541 GAQTPPRRSGRNAQAKKTDAVQIINAVGRPRRSKDRKTIGEQTANLİEEVTASNATVAAS 4600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99246063; PubMed=10231032;
Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
Nagase T., Ishikawa K.-I., Soyama M., Ohara O.;
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XIII.
The complete sequences of 100 new cDNA clones from brain which code for large proceins in vitro.";
DNA Res. 6:63-70(1999).
                                                                                                                                                                                              4497 SESC--NTRKSRRLOBKEDRSTVDDIIEDVVRNTNTPTGT------GPHLPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MINI HUMAN STANDARD; PRT; 3664 AA.
Q96758; Q9H9A8; Q9NWH5; Q9UQO1; Q9YSS6;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
MSX2-interacting protein (SMART/HDAC1 associated repressor protein).
MINI OR SHARP OR KIAA0929.
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4601 HLAPPEGAGVESHVPQLDAKEVEPVSVVTPIS-TPAPVSVAAPVTVPVPAMVP 4652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, INDUCTION, RNA-BINDING, AND INTERACTION WITH NCOR2; HDAC1; HDAC2; RBBP4; MBD3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 793-1595 FROM N.A., AND VARIANT PRO-1091.

TISSUE-Embryo, and Teratocarcinoma;

TISSUE-Embryo, and Teratocarcinoma;

TISSUE-Embryo, and Teratocarcinoma;

Nishikawa T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,

Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

Arita M., Nabekura T., Nagahari K., Masuho Y., Oshima A.;

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAR AND MTAILI.
TISSUE-liver, and Pituitary;
MEDLINE-21231190; PubMed=11331609;
Shi Y., Downes M., Xie W., Kao H.-Y., Ordentlich P., Tsai C.-C.,
Hon M., Evans R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                2770 HSSPSGTVAAR------VTPFNYNPSPRKSSADSTSARPSQIP
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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INTERACTION WITH PPARD.
MEDLINE=21874127; PubMed=11867749;
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Genes Dev. 15:1140-1151(2001).
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Adachi J., Aizawa K., Akimura T., Arakawa T., Carninci P., Fukuda S., Adachi J., Aizawa K., Akimura T., Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hirozane T., Hori F., Imorani K., Ishii Y., Itoh M., Kagawa I., Kojima Y., Kondo S., Konno H., Koya S., Miyazaki M., Murata M., Nakamura M., Nomura K., Numazaki R., Ohno M., Ohsato N., Saito R., Sakazume N., Sano H., Sasaki D., Sato K., Shibata K., Shiraki T., Tagami M., Takeda Y., Waki K., Watahiki A., Muramatu M., Hayashizaki Y.,
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TISSUB SPECIFICITY.
MEDLINE-22261914; PubMed=12374742;
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"SHARP is a novel component of the Notch/RBP-Jkappa signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [3]
SEQUENCE OF 69-3644 FROM N.A. (ISOFORM 2), AND VARIANTS THR-348;
PHE-762; PHE-773 AND LEU-933.
STRAIN-ICR; TISSUE-Brain;
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"MINT/Bpen negatively regulates Notch signaling by inhibiting RBP-3/Su(H) activity.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB-Cochlea;
MEDLINE=97237053; PubMed=9119401;
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Weil D., Pujol R., Petit C.;
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unconventional type I myosins.";
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ISSUE Brain;

MEDLINE=22579291; PubMed=12693553;

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Prediction of the coding sequences of mouse homologues of KIAA gene:

II. The complete nucleotide sequences of 400 mouse KIAA-homologous conna identified by sorrening of terminal sequences of conna candomly sampled from size-fractionated libraries.";
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MEDIJINE=2248365; PubMed=12594956;

Kuroda K., Han H., Tanigaki K., Tun T., Furukawa T.,

Kuroda K., Hani S., Tanigaki K., Tun T., Furukawa T.,

Taniguchi Y., Kurooka H., Hamada Y., Toyokuni S., Honjo T.;

"Regulation of marginal zone B cell development by MINT, a suppressor

of Norch/RBP-3 signaling pathway.";

Immunity 18:301-312(2003).

Immunity 18:301-312(2003).

-! FUNCTION: Essential corepressor protein, which probably regulates

different key pathways such as the Notch pathway. Negative
                                                                                                                                 [1] -
SEQUENCE OF 49-3644 FROM N.A. (ISOFORM 1), FUNCTION, SUBCELLULAR
LOCATION, TISSUE SPECIFICITY, DNA-BINDING, AND INTERACTION WITH MSX2.
Msx2-interacting protein (SMART/HDAC1 associated repressor protein). MINT OR SHARP OR KIAA0929.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                  MEDLINE=99379811; PubMed=10451362;
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The RRM domain of MINT, a novel msx2 binding protein, recognizes regulates the rat osteocalcin promoter.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 318-578 FROM N.A.
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EMBO J. 21:5417-5426(2002).
                                                                                                            NCBI_TaxID=10090;
    MINIT MOUSE STANDARD; PRT; 3644 AA. Q62504; Q80TN9; Q99PS4; Q9QZW2; 10-0CT-2003 (Rel. 42, created) 10-0CT-2003 (Rel. 42, last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update)
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regulator of the Notch pathway via its interaction with RBPEUH, which prevents the association between NOTCH1 and RBPSUH, and therefore suppresses the transactivation activity of Notch signaling. Blocks the differentiation of precursor B cells into marginal zone B cells. Probably represses transcription via the recruitment of large complexes containing histone deacetylase proteins. May bind both to DNA and RNA.

-!- SUBUNIT: Interacts with NOOR2, HDAC1, HDAC2, RBBP4, MBD3 and MTALL1. Interacts with he nuclear receptors RAR and PPARD. Interacts with RAR in absence of ligand. Bind to the steroid receptor RNA coactivator SRA (By similarity). Interacts with MSX2. Interacts with RBPSUH; this interaction may prevent the interaction between RBPSUH and NOTCH1.

-!- SUBCELLULAR LOCATION: Nuclear. Associates with chromatin.

Event=Alternative PRODUCTS:

Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BY726481; -; NOT ANNOTATED CDS.

R EMBL; AR55529; AAD55931.1; ALT_INIT.

R EMBL; AR55529; BA325731.1; ALT_INIT.

R EMBL; AK22402; BA3656.1; -...

R EMBL; AK22402; BA65684.2; ALT_SEQ.

R MGD; MGI:1891706; MIL.

R InterPro; IPR000504; RNA_rec_mot.

R SMART; SM00360; RRM; 3.

R PROSITE; PS50102; RRM; 4.

R PROSITE; PS50102; RRM; 4.

R PROSITE; PS50102; RRM; 4.

R PROSITE; PS50102; RRM; 7.

R PROSITE; PS60100; RPM RNP_1; FALSE_NBG.

R PROSITE; PS60100; RPM RNP_1; ALESE_NBG.

R PROSITE; PS60100; RPM RNP_1; ALESE_NBG.

R PROSITE; PS60100; RPM RNP_1; ALESE_NBG.

R PROSITE; PS60100; RPM RNP_1; ALESE_NBG.

R PROSITE; PS60100; RPM RNP_1; ALESE_NBG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Iso2d=262504-1; Sequence=Displayed,
Name=2;
Iso2d=262504-2; Sequence=VSP 008564;
Note=No experimental confirmation available;
Note=No experimental confirmation available;
Note=No experimental confirmation available;
Note=No experimental confirmation available;
Iso3DE SEPECIFICITY: Highly expressed in testie. Expressed at lower level in brain, lung, sphen, liver and kidney. Weakly expressed in cardiac and skeletal muscles and ovary. In spleen, it is marginal zone B-cells. While it is weakly expressed in DOMAIN: The RID domain mediates the interaction with nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: The SPOC domain, which mediates the interaction with NCOR2, is essential for the repressive activity (By similarity).
--- SIMILARITY: Belongs to the Spen family.
--- SIMILARITY: Contains 1 RIO (receptor interacting) domain.
--- SIMILARITY: Contains 8 RNA recognition motif (RRM) domains.
--- SIMILARITY: Contains 1 SPOC domain.
--- SIMILARITY: Contains 1 SPOC domain.
--- CAUTION: Ref.4 sequence differs from that shown due to multiple frameshifts and conflicts that create stop codons.
--- CAUTION: Ref.5 sequence differs from that shown due to what seems to be the presence of intronic sequence in the cDNA.
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2.9%; Score 428.5; DB 1; Length 3644;
Best Local Similarity 18.7%; Pred. No. 2.4e-08;
Matches 522; Conservative 325; Mismatches 903; Indels 1047; Gaps 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | :: | :: | : | : 277 KIGGNKIKVDFANRESQLAFYHCMEKSGQDMRDFYEMLTERRAGQMAQSKHEDWSADAQS 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :| | : | | : | | | | 340 VQNLPVRSIDTSIKDGEFHBFKKFĞKVTSVQIHGASERYĞLVFFRQQEDQEKALTASKG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 SSTASDDSPAR--------SVQSAAVPAPTSQLLSSLEKDEPRKSFGIK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----VSAIHTSQED-----RSSGSTT--ELHCVTDERNAL-----RRSSAAHTHSNT 934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        935 YNF------TKSEN-----SNRTCSM-----
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WITH MSX2.
WITH RBPSUH
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1053 KHIIEDEIKQS-EQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQQECVSPYRSR 1105	EQHEBEBRPTNYSIKYNBEKRHVDQPIDYSLKYATDIPS-SQKQS	778 YRRŚSERŚGSCŚSVGPPRYDKLEKARLERYŤKNEKADKĒRŤFDPĒRVERERRIVRKEKGE 837 1224 NAKRONOLHPSSAQSRSGOPOKAATCKVSSINQĒTIQTYCVĒDTPICFSRCSSLSSLSSA 1283	EDEIGCNQTTQEADSANTLQIAEIKEKIGTRSAEDPVSEVPAVSQHPRTKSSRL:::::	1338 QGSSLSSESARHAAVEFSSGAKSPEKSG	996 KLEARKRRFADSGLKIEKQKPEIKKTSPETEDTRILLKKÇPDTSRDGVLLREGESERK 1053 1387CTSVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSP 1427 1361 PARTE TEDEVICATE TO NOT SPENDENCE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVICE TO SERVE TEDEVIC		1488 LLHFATESTPDGFSCSSSLSALSLDE-PFIQKDVELRIMFPVQENDNGNETESEQPKESN 1546	1547 ENQEKEAEKTIDSEKDLLDDSDDDDIEILEECIISAMPTKSSRKAKKPAQ 1596 ::  : : :	1597 TASKLPPPVARKFSQLPVYKLLPSQNRLQPQKHVSFTPGDDMPRVYCVEGTP 1648	1649 1665 	1666PNBLAAGEGVRGGAQSGEFEKRDIIPTEGRS-TDEAQGGKTSS-VIIFELD 1714	1715DNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSAPNKN 1763 1423 LRDRDÇKLRERDERLASSLERNKFYS-FALDKTITPDTKALLERAKSLSSSREENWS 1478	1764OLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKN 1797 :                     1797 1479 FLDWDSRFANFRNNKDKEKVDSAPRPIPSWYMKKKKIRTDSEGKLDDKKDERREEEQERQ 1538	1798 NIMAERVFSDNKDSKK-QNIKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTFIEGTF 1853	ICF OKNUOLOGLOFUUTUUUVULGARENAELKKARENAEGEAR
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2597
                                             2720 NRLNSFIQVDAPDQK-GTEIKPG-----QNNPVPVSETNESSIVERTPPSSSSSKHSSP 2773
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                                                                                   TISSUE=Lens epithelium;

MEDIINE=90527161; PubMed=1694016;

MEDIINE=90527161; PubMed=1694016;

Makamura T., Donovan D.M., Hannada K., Sax C.M., Norman B.,

Flanagan J.R., Ozato K., Westphal H., Piatigorsky J.;

"Regallation of the mouse alpha A-crystallin gene: isolation of a constitution of a cis sequence motif shared with the major histocompatibility complex class I gene and other genes.";

Mol. Cell. Biol. 10:3700-3708(1990).

-i. FUNCTION: TRANSCRIPTION FACTOR WHICH BINDS SPECIFICALLY TO THE PALINDROMIC SEQUENCE 5'-GGGAAATCCC-3' IN THE ALPHA-A CRYSTALLIN
                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 40 (Transcription factor alphaA-CRYBPI) (Alpha A-Crystallin-binding protein I) (Alpha A-CRYBPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Nuclear.
-!- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE: THERE IS A FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brady J.P., Kantorow M., Sax C.M., Donovan D.M., Piatigorsky J.; "Murine transcription factor alpha A-crystallin binding protein I. Complete sequence, gene structure, expression, and functional inhibition via antisense RNA."; J. Biol. Chem. 270:1221-1229(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
----PPLEGVSAAAVPN----ADTQASE-
                                                                                                                                                                                   2774 SGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVN 2810
                                                                                                                                                                                                                                                                                                                              2688 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZINC-FINGER IN-BETWEEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95138112; PubMed=7836383;
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EMBL; 136825; AAA98810.1; JOINED.
EMBL; 136826; AAA98810.1; JOINED.
EMBL; 136827; AAA98810.1; JOINED.
EMBL; 136828; AAA98810.1; JOINED.
EMBL; X68946; CAA48762.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 2024-2688 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:96100; Hivepl.
InterPro; IPR007087; Znf C2H2.
Pfam; PF00096; zf-C2H2; 5.
                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
R PROSITE; PRODGS; ZnF_C2H2; 5.

R PROSITE; PS50157; ZINC_FINGER_C2H2_1; 4.

R PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.

W Transcription regulation; Zinc_finger; Metal-binding; DNA-binding;

W Nuclear protein; Repeat.

T ZN FING 407 429 C2H2_TYPE.

T ZN FING 415 459 C2H2_TYPE.

T ZN FING 435 459 C2H2_TYPE.

T ZN FING 435 976 C2H2_TYPE.

T ZN FING 953 976 C2H2_TYPE.

T ZN FING 2074 2096 C2H2_TYPE.

T ZN FING 2074 2096 C2H2_TYPE.

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T ZN FING 2074 2096 C2H2_TYPE.

T ZN FING 2074 2096 C2H2_TYPE.

T ZN FING 2122 C2H2_TYPE.

T ZN FING 2122 C2H2_TYPE.

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T ZN FING 2124 C2H2_TYPE.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.8%; Score 404; DB 1;
.8.4%; Pred. No. 1.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                         Pukuyama R., Rapoport S.I.;
"Brain-specific expression of human microtubule-associated protein 1A
"Brain-specific expression of human microtubule-associated protein 1A
(MAPLA) gene and its assignment to human chromosome 15.";
J. Neurosci. Res. 40.820-825(1995).
-!- FUNCTION: Structural protein involved in the filamentous cross-bridging between microtubules and other skeletal elements.
-!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate with MAPLA and MAPLA proteins.
-!- TISSUE SPECIFICITY: Brain.
                                                                                                                                                                                                                                                                                                                         -!- DOMAIN: THe basic region containing the repeats may be responsible for the binding of MAPIA to microtubules.
-!- PTM: Various serine residues may be phosphorylated by CAMP kinase.
-!- PTM: LC2 IS COEXPRESSED WITH MAPIA. IT IS A POLYPEPTIDE GENERATED FROM MAPIA BY PROTECLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH BOTH MAPIA AND MAPIB.
-!- SIMILARITY: TO MAPIB.
                          Obtani K., Rutherford T., Sakamoto H., Naftolin F.; "Microtubble associated protein 1A (MAP1A) in human brain sequence and physiological role."; Submitted (NOV-1996) to the BMBL/GenBank/DDBJ databases.
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                                                                                       SEQUENCE OF 134-419 FROM N.A.
IISSUE=Fetal muscle;
Chiannilkulchai N., Pasturaud P., Richard I., Auffray C.
                                                                                                                                Beckmann J.S.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 600178; -.
GO; GO:0005875; C:microtubule associated complex; TAS.
Mocrotubule; Repeat; Phosphorylation.
CHAIN ?2490 2805 MAP1 LIGHT CHAIN LC2.
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A -> G (IN REF. 4).
C -> A (IN REF. 3).
S -> G (IN REF. 3).
K -> G (IN REF. 3).
AK -> ST (IN REF. 1).
AK -> ST (IN REF. 1).
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9 X 3 AA REPEATS OF
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TISSUE=Brain;
MEDLINE=95356255; PubMed=7629894;
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SEQUENCE OF 78-1687 FROM N.A.
TISSUE=Brain;
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EMBL; U38292; AAB41133.1; -.
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E -> D (IN REF. 3).

E -> D (IN REF. 3).

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TK -> SG (IN REF. 3).

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TYLPGAITSPD -> EVLIWGDHQALN (IN REF. 3).

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G -> V (IN REF. 1).

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2.8%; Score 401.5; DB 1;
Best Local Similarity 18.2%; Pred. No. 1.7e-07;
Matches 523; Conservative 382; Mismatches 1149;
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2010	KSFHVEDTPVCFSRNSSLSSLSIDSEDDLIQECISSAMPKKKKFSRLKGDNEXHS 2064
1920	PRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSSNFDWKAIQEGAN 2109
2110	SIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPFTSNKGP 2165QMNLTGLGPACPTREPPLGAAGDWPPCLSTKEAAAGRNTSAEKELSSPISP 2023
2166	RILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQPLQANMPSIS 2225
2226	RGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGGTATTSPRGAKPSVK 2279
2280	SELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQS 2323 
2324	PGRNSISPGRNGISPPSPG 2370   :
2371	ROMSQONLTKQTGLSKNASSIPRSES-ASKGLNQMNNGNGANKKVELSRMSSTKS 2424 
2425 2256	SGSESDRSERPVIJVRQSTFIKEAPSPTLRRKLEESASFESLSPSSR 2470
2471	PASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGMRKLPPNLSPTIEYNDG 2520
2521	RPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSA 2576
2577	SSE- 
2618	NEFSPTNSTSQTVSSGATNGABSKTLIYQMAPAVSKTEDVWVRIEDCP 2665
2666	INNPRSGRSPTGNTPPVIDSVSEKANFNIKDSKDNQAKQNVGNGS 2710 
2711	VPMRTVGLENRLNSFIQVDAPDQKGTEIKPGQNNPVEVSETNESSIVERTPFSSSSSKH 2770
2771	SSPSGTVAARVIPENYNPSPRKSSADSTSARPSQIPTPVNNNTKKRDSKTDGTESSG 2827

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HSSP; P42771; IDC2.
Genew; HGNC:493; ANK2.
MIM; 106410; -.
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMB outstation. the Buropean Bioinformatics Institute. There are extrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=5;
Isoid=Q01484-3; Sequence=VSP 000268;
-: TISSUE SPECIFICITY: Plasma membrane of neurons as well as glial
cells throughout the brain.
-: PTM: Phosphorylated at multiple sites by different protein kinases
and each phosphorylation event regulates the protein's structure
and function (Potential).
-: SIMILARITY: Contains 23 ANK repeats.
                                                                                                                                                                                                                                                                                                                                                          Chan W., Kordeli E., Bennett V.; A440-kD annyring structure of the major developmentally regulated domain and selective localization in unmyelinated axons:"; J. Cell Biol. 123:1463-1473(1993).
                                                                                                                               Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 463-495 FROM N.A.
MEDLINE=92009921; PubMed=1833308;
TSE W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
Lux S.E., Ward D.C., Forget B.G.;
"Isolation and chromosomal localization of a novel nonerythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ankyrin gene.";
Genomics 10:858-866(1991).
-!- FUNCTION: Attach integral membrane proteins to cytoskeletal
-!- Alto bind to cytoskeletal proteins.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                   MEDLINE=91302466; PubMed=1830053;
Otto E., Kunimoto M., McLaughlin T., Bennett V.;
"Isolation and characterization of cDNAs encoding human brain
ankyrins reveal a family of alternatively spliced genes.";
J. Cell Biol. 114:241-253(1991).
                                           001454; 001485; 01486; 01486; 01486; 01-APR-1993 (Rel. 25, Created) 01-CT-1996 (Rel. 34, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, Pankyrin)
                                                                                                                                                                                                                                                                                       Carpenter S.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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                                   PRT; 3924 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q01484-1; Sequence=Displayed;
                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3) TISSUE=Brain stem;
                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain stem;
MEDLINE=94075409; PubMed=8253844;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
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                                   STANDARD;
                                                                                                                    Homo sapiens (Human)
                                   HUMAN
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2 -> QFLGKLHLPTAPPPLNEGESLVSRILQLGPPGTK
(in isoform 2).
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llarity 19.5%; Pred. No. 3.1e-07;
Conservative 311; Mismatches 803; Indels 644;
DR InterPro; IPR002110; ANK.

DR InterPro; IPR002010; Dath.

DR InterPro; IPR000906; Dath.

DR Pfam; PF00023; ank; 24.

DR Pfam; PF00031; death, 1.

DR PRINTS; PR01415; ANKYRIN.

SWART; SW000246; ANK; 22.

NR SWART; SW000246; ANK, 22.

NR SWART; SW00005; DEATH, 1.

R PROSITE; PS50037; ANK REPEAT; 20.

R PROSITE; PS50037; ANK REPEAT; 2.

R PROSITE; PS50037; ANK REPROSIO; I.

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R PROSIDE; PS50037; ANK REPROSIO; ANK I.
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LINK 2.
EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
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3562 AA; 388078 MW; 9BC566E88C1602D2 CRC64;
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PFam; PF00084; sushi; 1.

Pfam; PF00193; Xlink; 2.

PRINTS; PR01265; Link; 2.

SMART; SM00031; Link; 2.

SMART; SM00034; CLECT; 1.

SMART; SM0019; EGF CA; 1.

SMART; SM0019; EGF CA; 1.

SMART; SM0019; EGF CA; 1.

SMART; SM00419; IG; 1.

SMART; SM00449; IIK; 2.

PROSITE; PS00011; CTYPE LECTIN 1; 1.

PROSITE; PS00012; EGF 2; 1.

PROSITE; PS00022; EGF 2; 1.

PROSITE; PS00025; EGF 2; 1.

PROSITE; PS00025; EGF 2; 1.

PROSITE; PS00025; EGF 2; 1.

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       SEQUENCE FROM N.A. (ISOFORMS, VO AND V1).

STRAIN=White legion: TISSUB=Limb bud;

MEDLINE=93300846; PubMed=8314802,

A Shinomura T., Nishida Y., Ito K., Kimata K.;

Shinomura T., Nishida Y., Ito K., Kimata K.;

Shinomura T., Nishida Y., Ito K., Kimata K.;

Shinomura T., Nishida Y., Ito K.,

"CDNA cloning of FG-M, a large chondroitin sulfate proteoglycan

sopied during chondrogenesis in chick limb buds. Alternative

spliced multiforms of FG-M and their relationships to versican.";

J. Biol. (Chem., 268:1446-14469(1993).

-!- FUNCTION: May play a role in intercellular matrix. May take part in

the regulation of cell motility, growth and differentiation. Binds

hyaluronic acid.

-!- SUBCELLULAR LOCATION: Secreted, extracellular matrix.

-!- ALTERNATIVE PRODUCTS:

Event-Alternative splicing; Named isoforms=2;

COmment-Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        developing limb buds.
DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                 PECV CHICK
D PGCV CHICK
AC 090953; 090945; STANDARD; PRT; 3562 AA.
AC 090953; 090945; Stated)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last amonotation update)
DE Versican core protein precursor (Large fibroblast proteoglycan)
DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (By similarity).
--- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
--- SIMILARITY: Contains 2 link domains.
--- SIMILARITY: Contains 2 ESF-like domains.
--- SIMILARITY: Contains 1 C-type lectin family domain.
--- SIMILARITY: Contains 1 Sushi (SCR) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=090953-2; Sequence=VSP 003093;
TISSUE SPECIFICITY: Prechondrogenic condensation area of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q90953-1; Sequence=Displayed;
       3195 VQTGDIPPLSG--VKQISCPDSSE 3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, X60226; CAA42787.1; --
FIR, A17171; A47171.
HSSP, P00740; LEDT.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR000152; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR00110; IG-Tike.
InterPro; IPR00110; IG-Tike.
InterPro; IPR001399; IG-Tike.
InterPro; IPR001399; IG-Cin_C.
InterPro; IPR0001399; InterPro; IPR0001399; InterPro; IPR0001399; InterPro; IPR0001399; ID-Ctin_C.
InterPro; IPR0001399; IG-Cin_C.
InterPro; IPR0001399; IG-Cin_C.
InterPro; IPR00059; EGF; 2.
Pfam; PF000059; IGCTin_C; 1.
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NCBI_TaxID=9031;
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Query		δŏ	942 NSNRTCSMPY
Match	best nocal Similarity 18.5%; Fred. No. 5.2e-07; Matches 605; Conservative 465; Mismatches 1261; Indels 939; Gaps 141;	<b>4</b> 0 · ·	
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: 2	TDVTEIETTVPOREGDISIVPVTVGSEDIGEMOVTDHTSFDS	QC	1863 KSELDEFGST
ò	LKSHSLTIVSNACGTLWNI.SARNDKDORALWDWGAVSMI.KNI.HSKHKMI2	δλ	1647 TPINFSTATS:
; <u>8</u>	INTEATURSTRASEVPPREISTRD-ODREIGTAMGSTLPVTSVONHEOKTTAGFESDOT	qq	1913 LFINEGSAEE
ò	MGSAAALRNIMANRPAKXKDANIMSPGSSI.PSI.HVPKOKAI.EAEI.D	Å	1690 IPTEG
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i 음	SLHLTGTPKABTATDOBBK	q <sub>Q</sub>	2024 -MSENVFSTE
ò	LNTTVLPSSSSSRGSLDSSRSEKDRSLFRRRGTGTGNVHPATTENPGTSSKRGTGTG	ò	1792 NADS-KUNLN
අු	-   :   :   :	qq	2082 SPESVVNNST
à	882 TTAAQIAKVMEEVSAIHTSOEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSE 941	δλ	1843 PHHYTPIEGT
; A	TLGASKTVPESSA	ପୁଣ	2122 LGKILMIE
		λö	1901 TSNQQSANKT

δ	942 NSNRTCSMPYAK	田
· 선	    	TDKTTVISDLTTSSISAVDKIQPTSASKPFVSSKSPRIIPBEDE 1319
ò	997 YGQYPADLAHKI	MDDNDG.
qq	1320EV	FILE SENTING STREET STR
ò	1057 EDEIKQSEQRQS	KHLKFQPHFGQ [
ф	1354. DKĖYFTSSTATAVARPTA	VARPTAPPTVMEATEALQPQE-VSPTSHPD 1394
ò	SOSUNGINGING SOS	SNHGINQNVSQSLCQEDDYEDDKPTNYSERYSEEEQHEEEERP 1159
QQ	1395 SGTDIRLYVIQI	YVIQITGNDTDHPVNEFLDLFSRHILPHAVDETHTDAESAQTEPCTSDSVQDS 1454
ò	1160 TNYSI	KYNEEKRHVDOPIDYSLKYATDIPSSQKQSFSFSKSSGQSSKTEH 1210
qq	1455 SEYILDPFFPN	PNFMDFBEBEBDCENTTDVTTPPALQFINGKQQVTSAPKSTKABBARSDQ 1514
δŏ	S	HPSSAQ-SRSGOPOKAATCI
qq	1515 IESVAHSKNVTFSQINETNTF	SQINETNTFIISETEASGTMQPSKAGEVMGAFEVTQPTADV 1567
ò	1270 CFSRCSSLSSLS	Š
q	1568AMLEPVYSGESEV-	
ζ	1330 PRIKSSRLQGSSL-	1
qq	1608 GTEESSTKDTKNLLLI	
ò	1387 CTSVSSLDSFES	H
q	1660 TISVPTILSVER	TISVPILLSVERSAVTAAPSADSDTATVGIDVXDLIPKGGTATPGNYXKSTI 1711
ò	1447 QTKREVPKNKAP	QTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQ 1480
qq	1712 KLDAEFPFESNP	DAEFPFESNPEATSHTTKPDMTASSFIVLEGSGDVEENSTLASAMTTETAVAETLSVQ 1771
λ̈́O	1481VLP-	-DADTILHFATESTPDGFSCSSSLSALSLDEPFIQKDVELRIMPP 1527
Ср	1772 DISLGSGIVLPI	DTSLGSGTVLPTEISVTISEITPALPGGTRILYSTFDQSSEATVSTNFVSEL 1823
δ	1528 VQENDNGNETES	SNE
Dp	1824 IMEQVVGSSVATEKKVE	FI
à	1588 SRKAKKPAQTAS	SRKAKKPAQTASKLPPPVARKPSQLPVYKLLPSQNRLQPQ-KHVSFTPGDDMPRVYCVEG 1646
QQ	1863 KSELDEFGSTIN	LDEFGSTINEV-RIVSQEPIPLREIVPITGTWHSEIKKVTAIPFLREK 1912
ò	1647 TPINFSTATSLS	TPINFSTATSLSDLTIESPPNELAAGEGVRGGAQSGEFEKRDT 1689
g	1913 LFINEGSAEEPA	DLFAGSPTRKVVSTDSPFTDSGSGDIDVITESATLTSVPSRSVIETQT 1972
ò	1690 IPTEG	RSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPK 1734
Dp	1973 VKHEGNINVISV	SVSLKNTTTEYEEHIGTGGEVTSVSSTG-SDGLTEESEVAIE 2023
ò	1735 GKSHKPFRVKKI	VQQASASSAPNKNQLD
Ob	2024 -MSENVFSTENQGE	GEPTQEAVPTYTAPSDIKSRL-GSRREVTSHVTPVIRTKDLETAEVTS 2081
ò	1792 NADS-KNNLNAE	NLKNNSKDFNDKLPNNEDRVRGSFAFD
gg	ጨ	IRAVAESTESKKG
ò	1843 PHHYTPIEGTPY	CFSRNDSLSSLDFDDDDVDLSREKAELRKAKENKESBAKVTSHTEL 1900
qq	2122 LGKILMIE	HGSGEELKVDSSTTKLMSNGPTEKLLGSHFSFFD 2163
δ	1901 TSNQQSANKTQA	TSNQQSANKTQAIAKQPIN-RGQPKPILQKQSTFPQSSKDI 1940

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Event=Alternative splicing; Named isoforms=2;
Name=1;
                                                                                            5085 AA
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EMBL, AF27534; AAF63196.1; -.
HSSP, P04410; IA25
GO; GO:0045202; C:synaptic junction; IDA.
GO; GO:0005509; F:calcium ion binding; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9JKS6-1; Sequence=Displayed;
                     2802 PSQIPTPVNNNTKKRDSKTDSTESSGTQSP
                                        SFSLPEVTNGSDFLIGTSVGSVEGTAVOIP
3175 LGPLLGQQEITTISSNIATNNTAPGN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS
                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                 Neuron 25:203-214(2000)
                                                                                                                                                                   Rattus norvegicus (Rat)
                                                                                                                                                                                                  NCBI_TaxID=10116;
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                                                                                                                             2940 KSASTEYEETDSVSLNSVSQNPKSSVTVWLVNGVSKYPEVIIPSTSSAKDSDQSDHSSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWRKIKENEFS----PINSTSQTVSS--GATNGAESKTLIYQMAPAVSK----TEDVWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 DRSTERERPRLSSAP----VSDSPNSIEVGVFKPDQEAVTMLTSSLEPLDRSLETQSAL
  1941 PDRGAATDEKLONFAI-ENTPVCFSHNSSLSSLSDIDOENNNKENEPIKETEPP--DSQG
                                             TSLOTVTDTEMEEKAANELTVTSFATNLPLS-----EDVHSWEDRP-REILPKAIESSG
                                                                        EPSK-POASGYAPKSFHVE--------DIPVCFSRNSS-----
                                                                                             2277 EATEDPFFISTQANHEHVEFLSVPTIRPHSEBNKVEAESDEKILLPFNNDRVTESAVIER
                                                                                                                                                          -----DSENFDWKA-IQEGANSI
                                                                                                                                                                      AAELTETAYSMATSSPALEEESSSHSNSKDKDITHYFLVIEDPYNKEMDHRRGENGTSRP
                                                                                                                                                                                                                                                             2513 LPTPGDVSLEESSHMLTTDDVTPVSVILSETPYLEMGKSLATSATKMPSRVLPESSGEGS
                                                                                                                                                                                                                                                                                     -----MKQPLQANMPSISRGRTMIHIPGVRNSSSSTSPVSKKG
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                                                                                                                                                                                                                                                                                                                                                                     DSTPSRPAQQPLSRPIQSPGRNSISPGRNGISPPNKLSQLPRISSPSTASTKSSGSGKMS
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                                                                                                                  --LSSLSIDS--EDDLLQECISS-----AMPKKKKPSRLKGDNEKHS-PRNMGGILGE
                                                                                                                                                                                                  2112 VSSLHQAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPFTSNKGPR----
                                                                                                                                                                                                                                             ILKPGEKSTLETKK------IESESKGIKGGKKVYKSLITGKVRSNSEISGQ--
                                                                                                                                                                                                                                                                                                        2573 GWDGVSDSFAPDTLTHSTAPSVMEVELTASS------HIPGVYSEVMTT-----
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                                                                                                                                                           DLTL--DLKDIQRPDSEHGLSP----
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-----NPYSNEQSTISSELLNTIELVTS 3223
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-!- SUBCELLULAR LOCATION: Concentrated at presynaptic side of synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (kat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2), AND INTERACTION WITH RABACI.
MEDLINE-20170257; PubMed-10707984;
Fenter S.D., Chung W.J., Zhai R., Cases-Langhoff C., Voss B.,
Garner A.M., Kaempf U., Kindler S., Gundelfinger E.D., Garner C.C.,
"Piccolo, a presynaptic zinc finger protein structurally related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3]

CALICUM-BINDING ACTIVITY, AND MUTAGENESIS OF ASP-4668; ASP-4674; VAL-4688; MET-4689; VAL-4690; SER-4691; GLN-4692; ASN-4693 AND ALA-4694.

MEDLINE-21181819; Pubmed=11285225; Gerber S.H., Garcia J., Rizo J., Suedhof T.C.;

"An unusual C(2)-domain in the active-zone protein piccolo:
"An unusual C(2)-domain in the active-zone protein piccolo:
"An unusual C(2)-domain in the active-zone protein piccolo:
"An unusual C(2)-domain in the active-zone protein piccolo:
"An unusual C(2)-domain in the active-zone protein piccolo:
"An unusual C(2)-domain in the active-zone protein involved in the
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-!- SUBUNIT: Interacts with Rabacl/Pral, RIMS2 and profilin (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              namica_09JKS6-2; Sequence=VSP 003930, VSP_003931; DOMAIN: C2 domain 1 is involved in binding calcium and phospholipids. Calcium binds with low affinity but with high specificity and induces a large conformational change. SIMILARITY: Contains 2 C2 domains. SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
Fenster S.D., Cases-Langhoff C., Gundelfinger E.D., Garner C.C.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9JKE6; Q9JLT1; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Piccolo protein (Multidomain presynaptic cytomatrix protein).
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1524 IMPPVQENDNGNETESEQPKESN------ENQEKEAEKTIDSEKDLLDDSDDDI 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KESEAKVTSHTELTSNQQSANKTQALAKQPINRGQPKPILQKQS------TFPQS 1936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         978 PPPAKVGKPPPSEPEKAVPAHK-----PDKTTKPKPACPLCRTELNLG-SOEPPNFN--T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1995 SQGEPSKPQASGYAPKSFHVEDTPVCFS--RNSSLSSLSIDSEDDLLQECISSAMPKKKK
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                                                                                                                                                                                                                                                                                                                                                                       OPOPPTATKPHHQQPGLAKPSAQQPTKSISQTVTGRPLQPPPTS-AAQTPAQGLSKTICP
                                                                                                                                                                                                                                                                                                                                                                                                                             --GEFEKRDTIP-----TEGRSTDEAQGGKTSSVTIPELDD------NKAEEGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                          645 EPKKPPEPKKPPPLVKQPTLHGPTPATAPQLPVABALPEPAPPKEPSGPLPEQAKAPVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----IPQNTEYRTRVRKNADSKNNLNAERVFSDNKDSKKQNLKNNSKDFNDKLPNNEDRV
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/FILG=VSP_003931.
D-As: COMFLETE LOSS OF CALCIUM-BINDING
AND CALCIUM-DEPENDENT PHOSPHOLIPID
BINDING ACTIVITY.
D-As: COMFLETE LOSS OF CALCIUM-BINDING
AND CALCIUM-DEPENDENT PHOSPHOLIPID
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VV-SSS: 10-FOLD INCREASE IN AFFINITY FOR
CALCIUM.
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20.0%; Pred. No. 8.9e-07;
ive 241; Mismatches 775; Indels 532; Gaps
GO; GO:0005544; F:calcium-dependent phospholipid binding; IDA.

GO; GO:0005522; F:profilin binding; ISS.

GO: GO:0005010; F:vycoskeleton organization and biogenesis; ISS.

GO; GO:0016080; P:synaptic vesicle targeting; NAS.

InterPro; IPR000478; PDZ.

InterPro; IPR000478; PDZ.

R InterPro; IPR000489; Znf_piccolo.

R Ffam; PF00599; Zzf_piccolo.

R Pfam; PF00599; Zzf_piccolo.

R Pfam; PF00515; Zzf_piccolo; Z.

SMART; SM00239; DDZ; 1.

R RPROSITE; PS00049; CZ_DOMAIN_1; 1.

R PROSITE; PS50004; CZ_DOMAIN_2; Z.

R PROSITE; PS50106; PDZ; 1.

R PROSITE; PS50106; PDZ; 1.

R R PROSITE; PS50106; PDZ; 1.

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ACTIVITY.
5085 AA; 552702 MW; SAIBB543201A7450 CRC64;
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C2 DOMAIN 2.
TXPIN -> SKRK (in isoform 2).
/FIId=VSP_003930.
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C4-TYPE (POTENTIAL).
C4-TYPE (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                       ---DSSPSHKKGESKQQRKARHRSHGPLLPTIEDSSEBEBERREBEEL---LKEQEKQREL 1742
                  2395 E-SASKGLNOMNNGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQSTFIKEAPSPTL- 2452
                                                                                                  PTIEYNDGRPAKRHDIARSHSESP---SRLPINRSGTWKREHSKHSSSLPRVSTWRRT-- 2567
                                                                                                                                                           1481 GSSSSDEYKQEDSQGSGEREDFIRKQIIEMSAD-EDASGSEDEEFIRSQLKEISGVGESQ 1539
                                                                                                                                                                               ------ATNGA 2638
1273 GSSKDGQGERSKEKTEKEEDKSDISSSQQPKSPQGLSDIGYSSDGISGSLGEIPSLIPSD 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | : | : : : : : : : | | : | | ESEELVVAGGGGGRRFKTIEL---NSTIADKYSSESSQKKTILYFDEEPELEMESLTDSP
                                                          2453 RRKLEESASFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLS
                                                                      GSSSS-----ILSASSESSEKAKSEDEKHVNS----ISGTKQSK
                                                                                                                                                                                                   1540 KRE-EAKGKGKGVAGKHRRITRKSSTSFDDDAGRRHSWHDEDDETFDESPELKFRETKSQ
                                                                                                                                                                                                                       ESKTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSK
                                                                                                                                                                                                                                                               2699 DNQAKQNVGNGSVPMRTVGLENRLNSFIQVDAPDQKGTEIKPGQNNPVPVSETNESSIVE
                                                                                                                                                                                                                                                                                                     2759 RIPFSSSSSKHSSPSGTVAARVIPFNYNPSPRKSSADSISARPSQIPIPVNNNIKKRDS
                                     -----kkdsfsqess-psspbdaklestvl----sileaqastlv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Prediction of the coding sequences of unidentified human genes. IX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 552-4404 FROM N.A.
Kraemer J., Wollam C., Wohldmann P., McGrane B.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                ENQVSAKGTWRKI - - KENEFSPTNSTSQTVSSG-------
                                                                                                                                                                                                                                                                                                                                                                                                                         09Y6V0; 043373; 060305; 09BVC8; 09U1V2; 09Y6U9; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) PICCOLO protein (Aczonin) (Fragments).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell Biol, 147:151-162(1999).
                                                                                                                                                                                                                                                                                   .656 EDRSR---GEGSSSLH----
                                                                                                                                                                                                                                                                                                                                               2819 KTDSTESSGTQSPK 2832
                                                                                                                                                                                                                                                                                                                                                                 1743 EQQQRKSSSKKSKK 1756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Human)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profile institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                          TISSUBE-12388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Rtausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Ratausberg R.L., Feingold E.A., Grouse L.H., Schemen C.R., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheefer D. B., Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M., Vilalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Willalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rhiting M., Madan A., Young A.C., Shevchenko Y., Bulterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Thuman and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kalicki J., Elliott G.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: May act as a scaffolding protein involved in the organization of synaptic active zones and in synaptic vesicle trafficking (By similarity).

-!- SUBMIT: Interacts with Rabacl/Pral, RIMS2 and profilin (By similarity).

-!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isold=Q9Y6V0-2; Sequence=VSP_003923, VSP_003925, VSP_003925, VSP_003925, VSP_003925,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note=No experimental confirmation available;
DOMAIN: C2 domain 1 is involved in binding calcium and
phospholipids. Calcium binds with low affinity but with high
specificity and induces a large conformational change.
SIMILARITY: Contains 2 C2 domains.
SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synaptic junctions (By similarity).
ALTERNATIVE PRODUCTS:
Bvent-Alternative spliting; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P04410; 1A25.
Genew; HGNC:13406; PCLO.
Min, 604918; -
GO; GO:0005856; C:cytoskeleton; NAS.
GO; GO:0045202; C:synaptic junction; ISS.
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The complete sequences of 100 new cr code for large proteins in vitro."; DNA Res. 5:31-39(1998).
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SEQUENCE OF 4405-5147 FROM N.A.
                                                                                                                                                                         SEQUENCE OF 4405-4439 FROM N.A.
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EMBL; AC004082; AAB97937.1;
PIR; T00634; T00634.
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us-09-442-489f-7.rsp

1134 DYEDDKPINYSERYSEEGHEEEERPINYS	1190 SQKQSFSFSKSSGQSSKTEHMSSSSENTSTPSSNAKRQ	442 QQPGSAKPSAQQPSPAKPSAQQFTKPVSQTGFG	1250 KVSSINQETIQTYCVEDTPICFSRC	491SQGLPKTICPLCNTTELLLHVPEKANFNTC				597 DAAPKQDLSKAPEPKKPPPLVKQPT	1416 GIISPSDLPDSPGQTMPPSRSKTPPPPPPQTAQTKREVPK	624 GSPSAKAKQPPEADSLSKPAPPKEPSVPSEQ	1476 VQRVQVLPDADTLLHFATESTPPGFSCSSSLSALSLDEP	670VKPTTDLVSSSATTKPDIPSS	1536 BIESEOPKBS		KIDSAKPSQSFPPIGEKVIPFDSKAIPRPA	1567 SDDDDIEILEECIISAMPTKSSRKAKKPAQTASK	757 DPVQKKĖĖPKKAQTKMSPKPDAKPMPKGŠP	1615YKLLPSQNRLQPQKHVS	808 PQEQSRRFSLNLGSITDAPKSQPTTPQETVTGKLFGFGA	1643 CVBGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQS	868 SGPGAPMKQAPAPS-QPPTSQGPPKSTGQAPPAPAKS	1703 GKTSSVTIPELDDNKAEEGDILAECINSAMPK(	925 APTVKRIETEKKPPPIKDSKSLTAEPQKAVLPTKU	1756 SSSAPWION	980 SKDPPNFNTCTECKNQVCNLCGFNPTPHLTENCQTQRAIS	1779 IPQNTEYRTRVRKNADS	:     :: 1040 MPVPTESSSQKTAVPPQVKLVKKQEQEVKTEAEKVILEK	1812 KKQNLKNNSKDFNDKLPNNEDRVRGS	: :   : :	1857 SRNDSLSSLDFDDDDVDLSREKAELRKAKENKESE	:           :           :         :         : :         : :       : :       : :       : :       : :       : :       : :         : :       : :       : :       : :       : :       : :       : :       : :       : :       : :       : :       : :       : :       : :     :     : :   :   : :     : :   :   : :   :   : :   :   : :   :   : :   :   : :   :   : :   :   : : :   : :   : : :   : :   : : :   : :   : :   : : :   : :   : : :   : : :   : : :   : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   :	1910 TQAIAKQPINRGQPKPILQKQSTFPQSSKDII	DKSDTSS	1947 -TDEKLQNFALENTPVCFSHNSSLSS	1277 FIDEKDILKGLKKDSFSQESSPSSPSDLAKLESTVLSIL:	1987IKETEPPDSQGEPSK
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GO; GO:0005509; F:calcium ion binding; ISS. GO; GO:0005544; F:calcium-dependent phospholipid binding; ISS. GO:0005522; F:xxofflim binding; Tec	kelecon organization and biogenesis; ISS. tic vesicle targeting; ISS.	maptotagmin. IN	OTAGEN		nding; Zinc; Metal-binding; Zinc-finger; icing.		P-A-K-P-Q-P-X. C4-TYPE (POTENTIAL).	C4-IYPE (POIENTIAL).	POLY-PRO, PDZ,	C2 DOMAIN 1. C2 DOMAIN 2.	S -> SGNGLGIRIVGGKEIPGHSGEIGAYIAKILPGGSAE	GIGALMEG (IN 18010rm 2). /FTIG-VSP 003927	A -> AFIDGIKVSAFIIGELQ (IN ISOIOYM 2). /FIId=VSP 003924.	G -> GQVMVVQNAS (in isoform 2).	TAHKS -> SKRRK (in isoform 2),	/FTId=VSP 003926. Missing (in isoform 2).	/FIId=VSP 003927. 563537 MW; CD5D849998CD3C CRC64:	Saga	44; Pred. No. 9.4e-07; - 313; Mismatches 959; Indels	KDANIMSPGSSIPSI.HVRKOKAI.EABI.G	HILL IN THE STATE OF THE STATE	VGO TVTVIN		CT DOCE CONTROLL TO THE CONTRACT OF COMMENTS OF COMMEN		LKEEHKSSMMFGFLSEVNALSAVSSV		NEWSCENICKE CONFESSION COND.	ASSISTANCE OF THE STANDARD STA	PEKIKSQPPGTGKPIQGPTQTPQTDHAKLPLQRD	3KRQQ-MKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDND	KGBSVAFSLFSFSKFFLQQFTFGKFFAQQPGHEKSQF	GELDIPINYSLKYSDEQLNSGRQSPSQNERWARPKHIIEDEIKQSEQRQSRNQST 1073 GPAKPBAOPSGLHKPLAOOPGHTVKPPVOPSGHTKPPAOP1.GPAXPDAOGGRASS	- DGFANAFFAQQIGGBNFGG	DEFENDENCY OF THE STANDARD OF THE SECOND STANDARD OF THE STAND	יייי איייי אייייי אייייי איייייי איייייי
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ONOLHPSSAQSRSGOPOKAATC 1249 CSSLSSLSSAEDEIGCNOTTOF 1295 REKRHVDQPIDYSLKYATDIPS 1189 SSRLQGSSLSSESARHKAVEFS 1355 DSFESRSIASSVQSEPCSGMVS 1415 KNKAPTAEKRESGPKQAAVNAA 1475 PFIQKDVELRIMPPVQENDNGN 1535 -NENQEKEAEKTIDSEKDLLDD 1566 ------FIPGDDMPRVY 1642 SGEFEKRDTIPTEGRSTDEAQG 1702 -GKSHKPFRVKKIMDQVQQASA 1755 ---OLDGKKKKPTSP----VKP 1778 | |: |: |: |: |KVKETLSMEKIPPMVTTDQKQE 1099 EAK---VTSHTELTSNOOSANK 1909 CIKMEGLESGIPQSLEKEDDKT 1216 --KNNLNAER----VFSDNKDS 1811 -FAFDSPHHYTPIEG--TPYCF 1856 LLEEKKP---TPEDKKLLPEAK 1156 IPDRGAA----- 1946 : | : LSDTGYSSDGISSSLGEIPSLI 1276 | : | : :| LEAQASTLADEKSEKKTQPHEV 1336 -IKETEPPDSQGEPSK------PQASGYAPKSFHVE 2015 GKPLQPPTVSPSAKQPP---- 490 KLPP---PVARK----PSQLPV 1614 ----LSDIDOENNNKENEP--- 1986 SPAKPSPQQP-----GSTKPPS 441 CTECOTTVCSLCGFNPNPHLTE 541 :| : || : | TSAVSKSSPQPQQTSPK----K 596 SKVQSQAEEKTTPPL----- 705 : | : :| : PGPSSESKGQKQV----- 756 ASIFSQASNLISTAĞQPGPHSQ 867 SIPVKKETKAPAAEKLEPKAEQ 924 LEKSPKPESTCPLC-KTELNIG 979 -----LH 623 ::[|| |: : QDKAPVADDKPKQPKM-----

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SPEQPKDQEKTQSLSETLEITISBEBIKESQEERKDTFKKDSQQDIPSSKDHKEKSEFVD 1396
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MEDLINE=22737999; PubMed=12853948;
Millier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
Magner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
Mylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
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Mylie K., Sekhon M., Miner T.L., Nash W.E., Cordes M., Du H.,
Bun H., Edwards J., Bradshaw-Cordum H., All J., Andrews S., Isak A.,
Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
A vanbrunt A., Nguyen C., Du F., Laughlin Kohlberg S.,
Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
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A tir-Wollam A.-M., Abbott A., Minx P., Maupin R., Strowmatt C.,
A latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
Mendl M.C., Yang S.-P., Schultz B.K., Wallis J.W., Spieth J.,
A hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis B.R.,
A lifton S.W. Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
Simms B., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
Baertsch R.A., Brent M.R., Rehelber E., Rick P., Burk P., Suyama M.,
Bailey J.A., Portnoy W.E., Torrents D., Chinwalla A.T., Gish W.R.,
Materston R.H., Milson R.Y., Eichler E.E., Green B.D.,
Materston R.H., Milson R.K.,
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MLL3 HUMAN STANDARD; PRT; 4911 AA.
Q8NEZ4; QBNC02; QBNDF6; Q9H9P4; Q9NR13; Q9P222; Q9UDR7;
10-OCT-2003 (Rel. 42, Last sequence update)
110-OCT-2003 (Rel. 43, Last annotation update)
Myeloid/lymphoid or mixed-lineage leukemia protein 3 homolog (Histone-lymphoid or mixed-lineage leukemia protein 3 homolog (Histone-lymphoid or mixed-lineage leukemia protein 3 homolog (Histone-lymphoid or mixed-lineage leukemia protein 3 homolog (Histone-lympholog)
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MEDLINE=21886622; PubMed=11891048;
MEDLINE=21886622; PubMed=11891048;
Mault M., Brun M.-E., Ventura M., Roizes G., De Sario A.;
"MLL3, a new human member of the TRX/MLL gene family, maps to 7q36,
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DNA Res. 7:143-150(2000).

DNA Res. 7:143-150(2000).

SEQUENCE OF 3193-3865 AND 4460-4911 FROM N.A.

TISSUB=Placenta;

TISSUB=Placenta;

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara Nishikawa M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara Prakahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE-21574953; PubMed=11718452;
Tan Y.C., Chow V.T.;
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                                                                                                                                                                                                                                                                          (Homologous to ALR protein).
MLL3 OR HALR OR KIAA1506.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: Highly expressed in testis and ovary, followed by brain and liver. Also expressed in placenta, peripherical blood, fetal thymus, heart, lung and kidney. Within brain, expression was highest in hippocampus, caudate nucleus, and expression was highest in hippocampus, caudate nucleus, and substantia nigra. Not detected in skeletal muscle and fetal liver. DOMAIN: The SET domain interacts with histone H3 but not H2A, H2B and H4, and may have a H3 lyaine specific methylation activity.

-!- DOMAIN: The SET domain interacts with histone H3 but not H2A, H2B and H4, and may have a H3 lyaine specific methylation activity.

-!- MISCELLANEOUS: Found in a critical region of chromosome 7, which is commonly deleted in malignant myeloid disorders. Partial duplication of the MLi3 gene are found in the juxtacentromeric region of chromosomes 1, 2, 13 and 21. Juxtacentromeric region of the MLi3 gene has generated the BAGE genes.

-!- SIMILARITY: Contains 1 DHHC-type zinc finger.

-!- SIMILARITY: Contains 1 RING-type zinc finger.

-!- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Activating signal cointegrator 2 belongs to a novel steady-state
Lee J.W.;
Lee J.W.;
Lee J.W.;
Lee J.W.;
Lee J.W.;
Complex that contains a subset of trithorax group proteins.";
Complex that contains a subset of trithorax group proteins.";
Mol. Cell. Biol. 23:140-149(2003).
Cell. Biol. 23:140-149(2003).
Cell. Biol. 23:140-149(2003).
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Cell. Biol. 23:140-149(2003).
Cell. Biol. 23:140-149(2003).
Cell. Biol. 23:140-149(2003).
Cell. Belongs to the ASC-2/NCOA6 complex.
Cell. Subunit of this complex.
Cell. Belongs to the ASC-2/NCOA6 complex.
Cell. Subunit Selenosyl-L-methionine + histone L-lysine.
Cell. Subunit Belongs to the ASC-2/NCOA6 complex.
Cell. Subunit Belongs to the ASC-2/NCOA6 complex.
Cell. Subunit Belongs to the ASC-2/NCOA6 complex.
Cell. Subunit RBD-3/NCOA6, the retinoblastoma-binding protein RBD-3/NCLA2 and MLL3, and ASL2/ASCL2. Interacts with histone H3.
Cell. Biol. 23:140-149(2003).
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Cell. Biol. 23:140-149(2003).
Cel
                                                                                                                                                                                                                                                                                                                                                                     INTERACTION WITH ASC-2/NCOA6 CONTAINING COMPLEX (ISOFORM 2).

TISSUB=Cervical carcinoma;

MEDINE=2231496; PubNed=12482968;

GOO Y.-H., Sohn Y.C., And D.-H., Kim S.-W., Kang M.-J., Jung D.-J.,

Kwak E., Barlev N.A., Berger S.L., Chow V.T., Roeder R.G.,

Azorsa D.O., Meltzer P.S., Suh P.-G., Song B.J., Lee K.-J., Lee Y.C.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., 
Yamanoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., 
Ninomiya K., Iwayanagi T. Iwayanagi T. Iwasuho Y., 
"NEDO human cDNA sequencing project."; 
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                        Duesterhoeft A., Lauber J., Mewes H.-W., Weil B., Wiemann S., Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=1;
IsoId=Q8NEZ4-1; Sequence=Displayed;
                                                                                                                                                                                                     SEQUENCE OF 3879-4911 FROM N.A.
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EMBL; AF264750; AAF74766.2; -.
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---SSTHSAPR 302
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COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
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COLLED COLL (POTENTIAL).
A.T HOOK (BY SIMILARITY).
GLN-RICH.
PRO-RICH.
ASP-RICH.
EMBL; AK022687; BAB14179.1; -. EMBL; AK075113; BAC11409.1; -. EMBL; AL833924; CAD38780.1; -.
                           HGNC:13726; MLL3.
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AC104692; -; NOT ANNOTATED CDS. AC005631; -; NOT ANNOTATED CDS. AB040939; BAA96030.2; -.

AC006017; AAD45822

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	303 RLISHLGIKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLLHG 362	790 DLPSHDMLHNYPS	363 NDKDSVLLGNSRGSKEARARASAALHNIIHSQPDDKRGRREIRVLHLLEQIRAYCET 419   :		879 IWSIKVGRGSGFPGKRRPRGAGLSGRGRGSKLKSGIGAVVLPGVSTADISSNKDDEEN 938	HYSITLRRYAGMALTNLTFGDVANKATL-CSMK	939 SMHNTVVVLFSSSDKFTLNQDMCVVCGSFGQGAEGRLLACSQC 980	524 G-CMRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKT 562  524 G-CMRALVAQLKSESEDLQQVIASVLRNLSWR		1032 YHTYCLDPPLQTVPKGGWKCKWCVWCRHCGATSAGLECEWQNNYTQCAPCASLSSCPV 1089	593	1090 CYRNYREEDLILGCRQCDRW-MHAVCQNLNTEEEVENVADIGFDCSMCRPYMPASNVPSS 1148	607 -CAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHR 653	1149 DCCESSLVAQIVTKVKELDPPKTYTQDGVCLTESGMTQLQSLTVTVPRRKRSKPKLKL 1206	654 QILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNFKDQEALWD-MGAVSM 706	1207 KIINQNSVAVLÕTPPDIQSEHSRDGEMDDSREGELMDCDGKSESSPEREAVDDETKGVEG 1266	PSLHVRKQKALEAELD	1267 IDGVKKRKRKPYRPGIGGFVVRQRSRTGQGKTKRSVIRKDSSGSISEQLPCRDDGW 1322	766 AQHLSETPDNIDNLSPKASHRSKQRHKQSLYGDYVFDTNRHD 807	SEQUETO LEVUES VS VIES I ENTRANTANTE EL FER EXENTE COLLEGA CONTOCA EL ENTRANTANTE EL FER EXENTANTANTE EL FER EXENTANTANTE EL FER EXENTANTANTE EL FER EXENTANTANTANTANTANTANTANTANTANTANTANTANTAN	808 -DNRSDNFNTGNM-TVLSPYINTTVLPSSSSSRGSLDSSRSEKDRSLERE- 855 	856RGIGLGNYHPATENPGTSSKRGLQISTT 883	1443 DILGIISDDLAKSVDHSDIGPVTDDPSSLPQPNVNQSSRPLSEEQLDGILSPELDKWVTD 1502	884 AAQIAKVM EEVSAIHTS	1503 GAILGKLYKIPELGGKDVEDLFTAVLSPANTOPTFLPQPPPTQLLPIHNQDAFSRMPLM 1562	907GSTTELHCVIDERNALRRSSAAHTHSNTYNFTKSE-NSNRTC 947	1563 NGLIGSSPHLPHNSLPPGSGLGTFSAIAQSSYPDARDKNSAFNPMASDPNNSWTS 1617				SNDSMKRQQQQDSIDP	1048 RWARPKHIIEDEIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPH 1092 : :  :
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1728	SRIDSELFKDPLKQRESEHEQEWKFRQQMRQKSKQQAKIEATQKLEQVKNEQQQQQQQQ 1
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1145	ERYSEEEQHEEEERPTNYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSKSSS 1202 ::::
1203	PSPMDPYAKWGTPRPPVGHSFSRRNSAAPVEN-CTPLSSVSRPLQWMETTANRPSP 1948
1244	QKAATCKVSSINQETIQTYCVBDTPICFSRCSSLSSLSSLSSBEGGNQT 1292
1293	TQEADSANTLQIAEIKEKIGTRSAEDPVSEVPAVSQHPRTKSSRL 1337
1338	QGSSLSSESARHKAVEFSSGAKSPSKSGAQTPKSPPEHYVQETPLMFSRC 1387
1388	TSVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGGTMPPSRSKTPPPP 1442
1443	PRPTIVDPYSQQPQTPRPSTQTDLFVTPVTNQRHSDPYAHPPGTPRPGISVPYSQPPATP 2225
1468	KQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSCS 1503 :
1504	SSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKES 1545   :   :
1546 2339	
1587	S-SRKAKKPAQTASKLPPPVARKPSQLFVYKLLPSQNRLQPQKHVSFTPQDDMP 1639   : :
1640	RVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAGGEFEKRDTIPTEGR- 1695
1696 2499	STD
1728	IBL
1775	pvkpIPQNTEYRTRVRKNADSKNNLN
1801	GSGOTTI
1842	SPHHYTPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAEL
2737	NLETNDP

8 8 8	RESULT 1 CENE HUM ID CEN AC P49 DT 01-	DE CEN ODE CEN OS HOM OC BUK	OX NCB RN [1] RP SEQ RC TIS RX MED RA Lia				RY MED RA LI						RA Bisi RT "Fa: RT and RT mic:	C C C - 1 - C C C - 1 - C C C C C C C C
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IDLINE-9843747; PubMed=9763420;

And G.K.T., Schaar B.T., Yen T.J.;

And G.K.T., Schaar B.T., Yen T.J.;

Albaracterization of the kinetochore binding domain of CENP-E reveals theractions with the kinetochore proteins CENP-F and hBUBRI.";

Cell Biol. 143:49-63(1998). Biol. Chem. 275:30451-30457 (2000).
- FUNCTION: Probably required for kinetochore function, involved in chromosome segregation during mitosis. Interacts with retinoblastoma protein (RB), CENP-E and BUBRI.
- SUBUNIT: Homo- or heterodimer. EQUENCE FROM N.A.

DILINE-95379848 PubMed=7651420;

ux X., Mandrin M.A., Chang K.-H., Liu C.-Y., Chen C.-F., Shan B.,
nnes D., Yang-Peng T.L., Lee W.-H.;
haracterization of a novel 350-kilodalton nuclear phosphoprotein
hat is specifically involved intitotic-phase progression.";
1. Cell. Biol. 15:5017-5029 (1995). CENP-E mo sapiens (Human). karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 'BI\_TaxID=9606; COUENCE OF 2194-3210 FROM N.A.

O., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., Joshi H.C.;

N novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal main sufficient for nuclear localization.",

ochem. Blophys. Res. Commun. 212:220-228(1995). SSUE=Breast carcinoma;
BDLINE=95348175; PubMed=7542657;
ao H., Winkfein R.J., Mack G., Rattner J.B., Yen T.J.;
sNP-F is a protein of the nuclear matrix that assembles onto netochores at late G2 and is rapidly degraded after mitosis.";
Cell Biol. 130:507-518(1995). 15
MANN
STANDARD; PRT; 3210 AA.
49454; Q13171; Q13246;
1 - FEB-1996 (Rel. 33, Created)
1-FEB-1996 (Rel. 33, Last sequence update)
5-MAR-2004 (Rel. 43, Last annocation update)
ENP-F Kinetochore protein (Centromere protein F) (Mitosin) (AH ANNESYLATION.

Diline=20459117; PubMed=10852915;

Annes D., Gray K., Carr D., Black S., Armstrong shar H.R., Vames D., Kirschmeler P., Rathesyl transferase inhibitors block the farnesylation of GENP-F and alter the association of CENP-E with the cortubules."; 3844 2815 KRDSKTDSTES-----SGTQSPKRHSGS 2837 3812 EKQNPAEGLQTLGAQMQGGFGCGNQLPKTDGGS QUENCE FROM N.A. ntigen). SNPF.

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us-09-442-489f-7.rsp

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1414 LQSEHKILHDQHCQMSSKMSELQTYVDSLKAENLVLSTNLRNFQGDLVKEMQLGLEEGLV 1473
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KLLTQM---ESEKENLQSKI---NHLETCLKTQQIKSHEYNERVRTLEMDRENLSVEIRN 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEVAETS----QRISKLQEDTSAHQNVVAETLSALE----NKEKELQLLNDKVETEQAE
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                                                                                                                                                                                                SCISMRQSGCLPLLIQLLHGNDKDSVLLGNSRGSKEARA-RASAALH----NIIHSQPDD
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                                       231 IRQLLQSQATEAERSS-----QNKHETGSHDAERQNEGQGVGEINWATSGNGQGSTTRM
                                                                                                                   DHETASVLSSSSTHSAPRRLTSHLGTKVEMVYSLLSMLGTH---DKDDMSRTLLAMSSSQD
                                                                                                                                                      398 KRGRREIRVLHLLEQIRAYCETCWEWQEAHEPGMDQDKNPM-PAPVEHQICPAVCVIMKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1206 SKTEH------MSSSSENTSTPSSNAKRONOLHPSSAOSRSGO-----
                                                                             LHNVLDSKSVEVETQKLAYMELQQKAEFSDQKHQKEIE-----NMCLK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1010 SISELSDQ-----YKQEKLILLQRCEETGNAYEDLSQKYKAAQ--
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                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAMASSGQI
        -!- SUBCELLULAR LOCATION: Nuclear matrix (but not in the nucleolus), reorganization to the kinetochore/centromere (coronal surface of the outer plate) and the spindle during mitosis.
-!- DEVELOPMENTAL STAGE: Gradually accumulates during the cell cycle.
-!- PIWH: Hyperphosphorylated during mitosis.
                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 600236; -.
GO; 0005659; C:kinetochore; TAS.
GO; 0005651; C:nucleus; TAS.
GO; GO:0005631; C:spindle; TAS.
GO; GO:000067; P:DNA replication and chromosome cycle; TAS.
GO; GO:0000067; P:DNA replication of mitosis; TAS.
GO; GO:0007088; P:regulation of mitosis; TAS.
Mitosis; Phosphorylation; Antigen; Cell cycle; Repeat; Polymorphism;
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L -> Q (IN REF. 3).
D -> N (IN REF. 3).
ELNERVAALHNDQEACK -> SSMREWQPCIMTKKPVS
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2 X 177 AA TANDEM REPEATS.
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K -> N (in dbSNP:7289).
/FIId=VAR 014839.
T -> A (IN REF. 2).
G -> D (IN REF. 2).
MISSING (IN REF. 2).
MISSING (IN REF. 2).
V -> A (IN REF. 2).
V -> A (IN REF. 2).
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llarity 17.9%; Pred. No. 1.3e-06;
Conservative 502; Mismatches 1243;
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EMBL; U30872; AAA82935.1; -.
EMBL; U25725; AAA86889.1; -.
PIR; PC4035; PC4035.
Genew; HGNC:1857; CENPF.
GK; P49454; -.
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	2050 KKKPSRLKGDNEXHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFDWKAIQEGAN 2109 	g g
	1996 QGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPK 2049  1	\$ 8 8
Search completed: August 25, 2004, 17:17:17 Job time : 77.5 secs	1945AATDEKLONFALENTPVCFSHNSSL-SSLSDIDQE-NNNKENEPIKETEPPDS 1995 	S S
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Db 3095 PYILRRITHATRIPPRLAAQKLAI	2125DKTHDKTH	5 A
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QY 2707 -GNGSVPMRTVGLENRINSFIQVDAPDG	1772 PTSPVKPIPQNTEYRTRVRKNADSKNNLAMERVFSDNKDSKKQNLKNNSKDFNDKLPNNE 1831	δλ
2977 LETQVAHLCSQQSKQDSRGSP	1738HKPFRVKKIMDQVQQASASSSAPNKNQLDGKKKK 1771	& g
Db 2917 AAQEKQKTGTVMDTKVDELTTEIKELKETLE		qq
Qy 2625 STSQTVSSGAINGAESKTLIYQMAPAV-		ð
CY 2597 GTKQSKENQVS;  Db 2858 ATTQILEELKKTKOMDNLKYVNQLKKENE-R2	1663 BSPRNEL P 1684	à é
Db 2798 RLHEAEKKHQALLLDINKQYEVBIQTYREKI	1604 FVARKEDOLEVIKALLESONKLOF-OKHVSTTEODDMFRYZVEGTPINFSTATSLSDLTI 1662  1847FSGPNALVPMDFLGNÓSDIHNLÓLRVKETSNENLRLHVIEDRDRKV 1893	S G
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QY 2503 GWRKLPPNLSPTIEYNDGRPAKRHDIARSHG	QEKEAEKTIDSEKDLLDDSDDD1EILEECIISAMPTKS	δ
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Db 2630 QEQLVSKLSQVEGEHQLWKEQNLELRNITTV	1435 RSKTPPPPPQTAQTKREVPKNXAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLL 1489   :	8 S
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2334		<u>ያ</u>
Qy 2274 AKPSVKSELSPVARQTSQIGGSSKAPSRSGI		ò
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Qy 2154 QEEKPFTSNKGPRILKPGEKSTLETKKIES		,

2393 2154 QEEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQM 2213 2214 KOPLOANMPSISRGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGQTATTSPRG 2273 2394 SESASKGLNOM------NNGNGANKKVELSRMSSTKSSGSESDRSERPVLVROSTFI 2444 2445 KEAPSPTLRRKLEESASFESLSPSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQ--AG 2502 : | | : : | : : | 2687 ------KNLENELELTKWDKMSFVEKVNKMTAKETELQREMHEMAQKTAELQEELSG 2737 2738 EYNRLAGELQLILEBIKSSKDQLKELTLENSELKKSLDCMHKDQVEKEGKVREEIAEYQL 2797 2551 ----HSKHSSSL-----PRVSTWR-RIGSSSSILSASSESSEKAKSEDEKHVNSIS 2596 2597 GTKQ------RKIKENBESPTN 2624 2858 ATTQILEELKKTKMDNLKYVNQLKKENE-RAGGKMKLLIKSCKQLEEEKEILQKELSQLQ 2916 2625 STSQTVSSGA---TNGAESKTLIYQMAPAV---SKTEDVWV--------RIED---- 2663 2664 ------CPINNPRSGR----SPIGNIPPVIDSVSEK--ANPNIKDSKDNQAKONV-- 2706 2977 LETQVAHLCSQQSKQDSRGSPLLGPVVPGPSPIPSVTEKRLSSGQNKASGKRQKSGGWE 3036 2707 -GNGSVPMRTVGLENRLNSF1QV---DAPPOCKGTEIKPGQNNP------VPVSETNE 2753 2754 SSIVERTPESSSSSKHSSPSGTVAAR---VIPENYNPSPRKSSADSTS--ARPSQIP-- 2806 2798 RLHBABKKHQALLLDTNKQYEVBIQTYREKLTSKEECLSSQKLBIDLLKSSKEELNNSLK 2857 3095 PYILRRITMATRISPR------LAAQKLALSPLSLGKENLAESSKPTAGGSRSQKVKVA 3147 2274 AKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGR 2334 NGISPPNKLSOLPRISSPSTASTKSSGSKMSYTSPGROMSQONLTKOTGLSKNASSIPR 2494 INELQERESELE-----IINSSFENILQEREQEKVOMKEKSST------2503 GWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRL-----PINRSGTWKRE----3037 NGGGPTPATPESFSKKSKKAVMSGIHPAEDTBGTEFEP-EGLPEVVKKGFADIPTGKTS-2807 -- TPVNNNTKKRDSKTDST-----ESSGTOSPK 2832 : | | : | | : | | : | 3148 QRSPVDSGTILREPTTKSVPVNNLPERSPTDSPR 3181

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GenCore version 5.1.6
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,		time
1		Search
	OM protein - protein search, using sw model	August 25, 2004, 17:05:26 ; Search time 183.5 Seconds
	OM protein -	Run on:

(without alignments)
4888.383 Million cell updates/sec US-09-442-489F-7 14566 1 MAAASYDQLLKQVEALKMEN......ESSGTQSPKRHSGSYLVTSV 2843

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

1017041 segs, 315518202 residues

Searched:

1017041

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 25:\*
1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_tungi:\*
4: sp\_tuman:\*
5: sp\_invertebrate:\*
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sp\_virus:\*
sp\_vrebrate:\*
sp\_unclassified:\*
sp\_rvirus:\*
sp\_rvirus:\*
sp\_archeap:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			Description	P70039 xenopus lae	Q8bnp7 mus musculu	Q9z1k7 mus musculu	O95996 homo sapien	Q8brd8 mus musculu	Q9ubz1 homo sapien	Q9y632 homo sapien		Q9vas9 drosophila	Q9uem8 homo sapien	Q8c493 mus musculu	Q9y1t2 drosophila	Q961b0 drosophila	Q9p119 homo sapien	Q7z2q8 homo sapien	Q8c9i9 mus musculu
2717777		ı	ID	P70039	QBBNP7	Q9Z1K7	98880	Q8BRD8	Q9UBZ1	Q9Y632	P91667	Q9VAS9	Q9UEM8	Q8C493	Q9Y1T2	Q961B0	Q9P119	Q7Z2Q8	Q8C919
			DB	13	11	11	4	11	4	4	'n	Ŋ	4	11	w	Ŋ	4	4	11
			Match Length DB	2829	1056	2274	2303	489	733	1246	2416	2417	1685	324	1067	1067	208	159	146
	dР	Query	Match	72.4	35.4	24.1	23.4	15.3	14.9	13.7	12.2	12.1	11.7	8.6	8.4	8.4	7.1	5.2	4.7
			Score	10544	5162	3512.5	3415.5	2232	2170.5	1991.5	1780.5	1765	1705	1252	1222.5	1221.5	1041	756	680
		Result	No.	1	Ν	m	4	Ŋ	9	7	89	6	10	11	12	13	14	15	16

Q8ir22 drosophila O76891 drosophila Q9w596 drosophila Q8cmu7 staphylococ Q9uha8 homo sapien Q8bti8 mus musculu	Q9haw6 homo sapien Q9vc00 drosophila Q8vq99 staphylococ Q9v736 drosophila Q9uq35 homo sapien	4.60	062302 caenorhabdi Q9kx33 streptococo Q8isf6 caenorhabdi Q8isf7 caenorhabdi Q9v7g8 drosophila Q8mld9 drosophila	യഥ
Q81R22 O76891 Q9W596 Q8CMU7 Q9UHA8 Q8BTI8	Q9HAW6 Q9VC00 Q8VQ99 Q9V736 Q9UQ35	Q99QY4 Q8NUJ3 Q81FX6 Q21227 Q7ZA38 Q7XXN1	062302 Q9KX33 Q8ISF6 Q8ISF7 Q9V7G8	29 VALU 293 9NS 29 KWR3 28 TZM8 29 FNDS 27 YZH1
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## ALIGNMENTS

Oy 1249 CKVSSINQETIQTYCVEDTPIC	Qy 1308 KEKIGTRSAEDPVSEVPAVSQi 	OTPKSPPEH           OTPKSPPEH	1426 SPGQTMPPS           1433 SPGQTMPPS	1486 DTLLHRATESTPDG 	1546	1607 V	1667 PPSE-PIND	1725	1785	1841	1901	1964 SHNSS 	2021	2082 D 2081 D	2142 ISLGSPFHL          2141 ISLGSPFHL	Db 2201 KSRSSDFSSHCKQSVQTNMPF	2262	Qy 2322 QSPGRNSISPGRNGISPDNKL
181 QTDMTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT 240 181 QTDMTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT 240 181 QTDMTRRQLIRVERQLIRVERQLIGTCQNGMEKRAQTRYGKTHQIRFETIRIRGLIQSQVA 240	E-AERSSQNKHETGSHDAERQNEGQGGGEINMATS-GNGQGSTTRWDHETASVLSSSSTH 29  E-AERSSQNKHETGSHDAERQNEGQGVGEINMATS-GNGQGSTTRWDHETASVLSSSSTH 29  E-AERSSQNKHETGSHDAERQNEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	SAPRILISHLGTKVENVYSLLSVLGTHDKDDMSRTLLAMSSSQDSCISNRQSGCLPLLIQ 35	LLHGNDKDSVLLGNSRGSKEARARASAALHNI IHSQPDDKRGREIRVIHLLEQIRAYCE	419 TCWEWQEAHEDGMDQDKNPMPAPVEHQICPAVCYLMKLSFDEEHRHAMNELGGLQAIAEL 478 	479 LQVDCEMYGLTNDHYSITLRRYAGMALTNLIFGDVANKATLCSMKGCMRALVAQLKSESE 538 	539 DLQQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWNLSAH 598 	599 CTENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRE 658 		719 ANGSAAALRNIMANRPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDN 778 	779 LSPKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSS 836      :	837 SRGSLDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKR-GLQISTTAAQIAKVMEBVS 895   ::	F 3	956 YKRSSNDSLANSVSSSDGYGKRGQWKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHWD 1015    :          ::        :	1016 DNDGELDTPINYSLKYSDEQLASGRQSPSQNERWARPKHIIEDBIKQSEQRQSRUGSTTY 1075 	1076 PVYTESTDDKHLKFQPHFGQQCCVSPY-RSRGANGS-ETNRVGSNHGINQNVSQSLCQED 1133 1076 SSYTENKEEKHKKFPPHFNQSENVPAYTRSRGANNQVDQSRVSSNLSNNSKAŠKPHCQVD 1135	1134 DYEDDKPTNYSERYSEEGHEEE-ERPINYSIK-YNEEKRHYDQPIDYSLKYATDIPSS- 1190   :      :	OKOSFSFSKSSGOGSKTEHMSSSENTSTPSSNAKRONOLHPSSAQSRGOPOKAAT 12	
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299 PRRITSHLGTKVEMVYSLLSMLGTHDKDDMSRTILLAMSSSQDSCISMRQSGCLPLLIQLL
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                             Length 1056
                                                                         Indels
                          35.4%; Score 5162; DB 11;
95.1%; Pred. No. 1.2e-245;
live 21; Mismatches 29;
                          Query Match
Best Local Similarity 95.1
Matches 1006, Conservative
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NUCRL_INALDELUCY;

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NUCRL_INECTREGORY;

NUCRL_INECTREGORY;

NUMBOLINE=2234683; PubMed=12466851;

NUMBOLINE=22354683; PubMed=12466851;

NUMBOLINE=22354683; PubMed=12466851;

NUCRL_RENG NEONORE EXPLORATION Research Group Phase I & II Team;

NUCRL_INECTREGORY;

NUMBOLINE=235483; PubMed=12466851;

NUMBOLY MGI:88039; Apc.

NUMBOLY MGI:88039; Apc.

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Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Musinse; Musinsi TaxID=10090;
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1-MAR-2003 (TIEMBLrel. 23, Last sequence update)
01-OCT-2003 (TIEMBLrel. 25, Last annotation update)
Adenomatosis polyposis coli (Fragment).
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NLIHSKHKMIAMGSAAALRNIMANRPAKYKDANI-MSPGSSLPSLHVRKQKALEAELDAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1173 VDQPIDYSLKYATDIPSSQKQSFSFSKSSSGQSSKTEHMSSSSSENTSTPSSNAKRONQLH
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                             LVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSV
                                                                                                                                                                                                                                                                                                                                            LSALWNISAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIAT
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                                                                           CLPLLIQLLHGNDKDSV---LLGNSRGSKEARARASAALHNIIHSQPDDKRGRREIRVLH
                                                                                                                                           LLEQIRAYCETCWEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNE
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MEDLINE=99147086; PubMed=10021369;
van ES J.H., Kirkpatrick C., van de Wetering M., Molenaar M.,
Miles A., Kuipers J., Destree O., Peifer M., Clevers H.;
"Identification of APC2, a homoloque of the adenomatous polyposis coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEA--MA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MGD; MGI:1346052; Apc2.
InterPro; IPR00838; ARM.
InterPro; IPR00825; Armadillo.
InterPro; IPR00825; Ppantne_S.
Pfam; PF00514; Armadillo_seg; 3.
SMART; SM00165; ARM; 5.
PROSTIE; PS00012; PHOSPHOPANTETHEINE; 1.
SEQUENCE 2274 AA; 243137 MW; 75ABDAISDOF707F5 CRC64;
1021 LDTPINYSLKYSDEQLNSGROSPSQNERWARPKHIIED 1058
1019 LDTPINYSLKYSDEQLNSGROSPSQNERWARPKHVIED 1056
                                                                                                                                                                 Last sequence update)
Last annotation update)
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AJ130783; CAA10207.1; JO
AJ130784; CAA10207.1; JO
AJ130785; CAA10207.1; JO
AJ130786; CAA10207.1; JO
AJ130789; CAA10207.1; JO
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AJ130799; CAA10207.1; JO
AJ130799; CAA10207.1; JO
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AJ130799; CAA10207.1; JO
AJ130799; CAA10207.1; JO
AJ130799; CAA10207.1; JO
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                                                                                                                  PRELIMINARY;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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L Cancer Ree. 58:176-5181(1998).

R EMEL, AB022529; BAA75469.1; JOINED.

R EMEL, AB022529; BAA75469.1; JOINED.

R EMEL, AB022521; BAA75469.1; JOINED.

R EMEL, AB022524; BAA75469.1; JOINED.

R EMEL, AB022524; BAA75469.1; JOINED.

R EMEL, AB022525; BAA75469.1; JOINED.

R EMEL, AB022525; BAA75469.1; JOINED.

R EMEL, AB022526; BAA75469.1; JOINED.

R EMEL, AB022528; BAA75469.1; JOINED.

R EMEL, AB022528; BAA75469.1; JOINED.

R EMEL, AB022528; BAA75469.1; JOINED.

R EMEL, AB022528; BAA75469.1; JOINED.

R EMEL, AB022528; BAA75469.1; JOINED.

R EMEL, AB022528; BAA75469.1; JOINED.

R EMEL, AB012162, BAA75469.1; JOINED.

R EMEL, AB012162, BAA75469.1; JOINED.
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Koyama K., Nakagawa H., Nakamura Y.;
"APCL exon14.";
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                              -----TPSSSSENCVQETPLVLSRCSSVSSLGSFESRS
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GO:0008013; F:beta-catenin binding; TAS. GO:0006641; P:procein complex assembly; TAS. GO:0007165; P:signal transduction; TAS. GO:0007165; P:signal transduction; TAS. TFP:0 IPR000225; Armadillo. TPF:0 IPR00181; Pept MIQA MIZB. TPF:0 IPR00181; Pept MIQA MIZB. TPF:051; PR001815; ARM; 5. TI: SM00185; ARM; 5. TI: PR00186; CYSTEINE SWITCH; 1. TENCE 2303 AA; 243946 MW; TBF940183ACD643D CRC64; Atch atch cal Similarity 34.4%; Pred. No. 3e-159;	97; Conservative 372; Mismatches 815; I 2 AAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASN :	64 LVSSGQTEVLEQLKALQMDITSLYNLKRQPPTLGPEPARITPEGSPV-HGSGP 115 120 RR-GEVNGSRESTGYLEELEKERSLILADLDKEEKEKDWYYAQLQNLTKRIDSLPLTE-N 177 116 SKDSFGELSRATIRLLEELDRERCFLLNEIEKERSKELMYYSQLQGLSKRLDELPHVETQ 175 118 FSLQTDMTRRQLEYBARQIRVABEQLGTCQDMEKRAQRILARIQQIEKDILRRQLLQS 237 119 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	176 FSMQMDLIRQQLEFEAQHIRSLMEERFGTSDEWVQRAQIRASRLEQIDKELLE 228 238 QATEAERSQNKHETGSHDAERQNEGGGGGEINMATSGNGGGSTTRMDHETASVLSSSST 297 229	263 DGTPOPGNSKVENVFWLLSMLATROGEDTARTLLAMSSSPESCVAMRSGCLPLLL 318 358 QLLHGNDKDSVLGNSRGSKEARARASAALTHINISQDDKRGRREIRVLHLLEQIR 414		594 NLSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHR 653	714 KHKMIAMGSAAALRNIMANRPAKYK-DANIMSPGSSLPSLHYRKQKALEAELDAQHLSET 772 679 KHKMIAMGSAAALRNILAHRPAKHQAAATAVSPGSCVPSLYYRKQRALEAELDARHIAQA 738 773 FDNIDNLSPKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTG 817 819 LEHLEKQGPPAAEAATKKPLPPLRHLDGLAQDYASDSGCFDDDDAPSSLAAAAATGEPAS 798 818NMTVLSPYLNTTVLPSSSSSRGSLDSSRSEKDRSLERBRGIGLGNYHPATENPGTS 873 818NMTVLSPYLNTTVLPSSSSSRGSLDSSRSEKDRSLERBRGIGLGNYHPATENPGTS 873

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WEDLINE-2234683; PubMed=12466851;
WEDLINE-22354683; PubMed=12466851;
The FANTOM Consortium,
The FANTOM Consortium,
The RAIREN Genome Exploration Research Group Phase I & II Team;
The RAIREN Genome Exploration Research Group Phase I & II Team;
The RIKEL, ARCHSOS; PAC22198.1;
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Mus musculus (Mouse).

Mus musculus (Mouse).

Musmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUB-Kidney;
MEDLINES99147086; PubMed=10021369;
van Es J.H., Kirkpatrick C., van de Wetering M., Molenaar M.,
Miles A., Kuipers J., Destree O., Peifer M., Clevers H.;
"identification of APC2, a homoloque of the adenomatous polyposis coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53; Gaps
                                                                                                Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

van Es J.H., Kirkpatrick C., van de Wetering M., Molenaar M.,
Miles A., Kirkpatrick C., van de Wetering M., Clevers H.;
Miles A., Kuipers J., Destree O., Peifer M., Clevers H.;
Adenomatous Polyposis Coli Homologs in Nammals and Flies.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ012652; CAB61207.1; -.
EMBL; AJ012652; AAF01784.1; -.
InterPro; IPR008238; ARM.
InterPro; IPR008238; ARM.
InterPro; IPR00825; Armadillo.
Pfam, PF00614; Armadillo.
Pfam, FR00185; ARM; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          tumour suppressor.";
Curr. Biol. 9:105-108(1999).
protein (Fragment)
                                                                Homo sapiens (Human)
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                                                                                                                                                                 NCBI_TaxID=9606;
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RA SEQUENCE FROM N.A.

RA Carr I.M., Markham A.F., Colleta P.L., Wai L., Askham J., Morrison E.,

RA Meredith D.M.;

RI "APC2 alternatively spliced cDNA sequence.";

RI "APC2 alternatively spliced cDNA sequence.";

RI "APC2 alternatively spliced cDNA sequence.";

RI "APC3 alternatively spliced cDNA sequence.";

RI "APC3 alternatively spliced cDNA sequence.";

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                                                  655 ILRENNCLOTLLOHLKSHSLTIVSNACGTLWNLSARNPKDOEALWDMGAVSMLKNLIHSK
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                                                                                                                                                                                                                                                                                                                                                                              715 HYMIAMGSAAALRNIMANRPAKYK-DANIMSPGSSLPSLHVRKQKALEAELDAQ 767
                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata, Vertebrata, Euteleostomi;
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.7%; Score 1991.5; DB 4; Length 1246; Best Local Similarity 30.5%; Pred. No. 1.5e-89; Matches 579; Conservative 193; Mismatches 428; Indels 697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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Oy 1415 SGIISPSDLPDSPGGTMPPSRSKTPPPPPQTAGTKREVPKNKAPTAEKRESGPKQAAV 1472	1473 NAAVQRVQVLPDADTLLHFATESTPOGESGSSLSALSLDEPFIQKDVELRIMPPVQ 15  968 IADCRERCELPAGS-VRFTVEKPDENFSCASSLSALALHEHTVQQDVBLRLLPSAC 10  1530 ENDNGNETESEQPKESNESCHENTDSEKDLLDDSDDDDIBLLEGGIISAMPTKSSR 15  1027 PERGGGAGGAGLHFAGHRRGGAGÄHGFSPSRRRGQELELLRECLIGAAVPARLEK 10	 1706 1175 1176 1176	1826 KLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRNDSL 1862 	PRT; 2416 AA. reated) ast sequence up	UL-CUI-ZOS (ITEMBLIZEL 25, ADENOMATOUS POLYPOSIS COLI. APC OR D-APC OR CG1451. Drosophila melanogaster (Fri Eukaryota, Metazoa, Arthrop Neoptera, Endopterygota, Di Ephydroidea, Drosophilidae, NCBI_TAXID=7227;	11) REQUENCE FROM N.A. MEDLINE-97144426; Pubmed=8990193; Hayashi S., Rubinfeld B., Souza B., Polakis P., Wie	KT "A Drosophila homolog of the tumor suppressor gene adenomations RT polyposis coli down-regulates beta-catenin but its zygotic expression RT is not essential for the regulation of Armadillo."; RL Proc. Natl. Acad. Sci. U.S.A. 94:242-247(1997). DR EMBL, U77947; Amal41404.1; DR PIR; 713825; 713825.	DR Plybase; FBgn0015589; Apc.  DR GO; O008013; F: beta-catenin binding; IDA.  DR InterPro; IPR008938; ARM.  DR InterPro; IPR000225; Armadillo.  DR Pfam; PF00514; Armadillo_seg; 5.  DR SWART; SMO188; ARM; 5.  DR PROSTTE: PS60176; APW PERPERP.	SEQUENCE 2416 AA; 261405 MW buery Match 12.2%; Sest Local Similarity 25.4%; Patches 720; Conservative 329; 243 ERSSQNKHETGSHDAERQN-E
168 167 359 LLHGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDDKRGRREIRVLHLLEQIRAYCE 418	168	289 STENKAAICQVDGALGFLVSTLTYKCQSNSLAIIESGGGILKNVSSLVATREDYKQVIRD 348 659 NNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSKHKNI 718 :	AMGSAAALRNLLAHRPAKHQAAATAVSPGSCVPSLYVRKQRALEAELDARHLAQALEHLE NLSPKASHRSKQNTGMYTVLS	SKRGLQI : : : AKAKAKL - NTYNFT	KSENSNRTCSMPYAKLEYKRSSNDSLNSVSSDGYGKRGQMKPSIESYSEDDESKFCSYG		1119 HGINQNVSQSLCQEDDYEDDKPTNYSERYSEEGHEEEERPTNYSIKYNEEKRHYDQPID 1178  692LDLDPPQCQAEPPAREATSADARVRTIKLSPTYGHV 727  1179 YSLKYATDIPSSQKQSFSFSKSSSGQSSKTEHMSSSSENTSTPSSNAKRQNQLHPSSAQS 1238		1299 ANTLQIAEIKEKIGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEF 1354  :::::::::::::::::::::::::::::::::::

			15/3 -EILEBEC.   :     1205 GHLLQQCC   631 SFTPGDDN   1245ADER				
90 A	À 9 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	8 6 8 6	3 A 3 A 3	3 6 5 6 5	2 4 4 4 4	6 6 6 6	6 6 6 6 6 6 6
:   :	338 SSSQDSCISMRQSGCLPLLIQLLHGNDXDSVLLGNSRGSKEARARASAALHNIIHSQPDD 397   :     :	LSFDEEHRHAMNELGGLQAIAELLQVDCEMYG-LTNDHYSITLRRYAGMALTNI/FGDVA		695 QEALMDMGAVSMLKNLIHSKHKVIAMGSAAALRNLMANRPAKKYDANIMSPG-SSL 749	810 RSDNFNTGNMTVLSPYLNTTVLPSSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATEN 869	726	1110 SETURVGSNHGINQNVSQSLCQEDDXEDDKFTNYSERYSEEGHEEERPTNYSIKXNBE 1169  779
96 AG	8 8 8	8 6 6 6	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	b oy b	6 6 6 6 6	8 6 8 6 8	, 6 2 6 2 6 6 6

0	925	SLDESGKANQAIVGTDADIKPKLEKQEEQESQPAEQVLTKPPTQANSAL 973
_	1338	QGSSLSSESARHKAVEFSSGAKSPSKSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFE 1397
0	974	
_	σ.	PCSGMVSGIISPSDLPDSPQQTMPPSRSKTPPPPPQTAQTKREV 145
٥		107
<b>~</b> 0	1453	PKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSSLSALSLD 1512 
>-	1513	EPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKE-AEKTID 1558
0	1092	Erir 114
<b>&gt;</b>	55	SLIDD-SDDDDI 1572
0 5	1573	163
. ۵	20	<b>X</b>
>-	1631	SFTPGDDMPRVYCVECTPINFSTATSLSDLTIESPPNELAAGEGVRGGAGSGEFEK 1686
Ω	1245	ADEMNK-FLUVEDSPCNFSVVSGLSNLTVGSSLVGPAVQLKETE-PSSADQNPEMKR 1298
>-	1687	RDIIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAEC
Ω	1299	SLANRSKSRRPPHWQDDSLSSLSIDSEDDTNLLSQAIAAGCNRPKSNLGFSSNGKRSSSL 1358
>-	1728	INSAMPKGKSHKPFRVKKIMDQVQQASASSAPNKNQLDGKK 1769
Д	1359	SSSQPIAINAATSASSLNSAMTVRKSQQQESYSSVDSSDSNDNQSKSLFELCILKGMYKT 1418
>-	1770	180
Q	1419	SSGQVKRQKHHHHHHHKEKEK 147
ъ а	1804	VFSDNKDSK-KQNLKONSKDFNDKLPNNEDRVRGSFAFDSPHYTPIEGTPYCFSRND 1860 :
>	1861	SREKAELR
Д	1524	
<b>*</b>	1919	-NRGOPKPILQKQSTFPQSSKDIPDRGAATDEKLQNPAIENTPVCF 1963
.α	1578	Н
λ.	1964	SLSDIDQENNNKENEPIKETEPPDS 19
q	1637	HKDPDLMLKSVERLTMEFVTSAEQLRSSSHNHSSSNSHKNNSSNNTWNESTCPND 1691
<u>~</u>	1996	QGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPKKK 2052
,q	1692	VSFPSVSQTAPVLASLSLDEDATEARSLHELIEITPTNEQQ 1732
<b>≱</b> •	2053	SRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFDWKAIQEGA 210
۾	1733	PESLEGETDTLYNGHADSYSGSSGGLNFQLGGQVQNAGVRLEPQRLLFNGTSASIMT 1789
<u> </u>	0	NSIVSEHQAAAACLSRQASDSDSILSLKSGI-SLGSPFHLTP 215
q	1790	NSTMIAFEARALAENILQPAATDDDTTEMTFSLNSLDLDNIRPPSGMESLNSCYQDHSQP 184
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۵	1850	SSLRQAMPS-KSPRFARKMFFANLVARKALGHLAGSAESVNSSCRLLLDN

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243 ERSSQNKHETGSHDAERON-EGOGVGEINMATSGNGOGSTTR-----MDHETASVLSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSSQDSCISMRQSGCLPLLIQLLHGNDKDSVLLGNSRGSKEARARASAALHNITHSQPDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 KRGRREIRVLHLLEQIRAYCETCWEWQEAHEPGM--DQDKNPMPAPVEHQICPAVCVLMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 LSFDEEHRHAMNELGGLQAIAELLQVDCEMYG-LTNDHYSITLRRYAGMALTNLTFGDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 VSFDEEHRHAMCELGALHAIPNLVHLDHAVHGPKPEDQCCNSLRRYALMALTHILFGGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         515 NKATICSMKGCMRALVAQIKSESEDLQQVIASVIRNISWRADVNSKKTIREVGSVKALME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410 NKALLCGOKOFMEALVAOLDSAPDDLLOVTASVLRNLSWRADSNMKAVLNEIGTVTALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470 AAMRNRSENTLKAILSALMNLSAHCSTNKAEFCAVDGALAFLVGMLSYEGPSKTLKIIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             635 GGGILRNVSSLIATNEDHRQILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPXD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   575 CALEVKKESTLKSVLSALWNLSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 25.3%; rred. NO. 3.55.70, 100 Conservative 325; Migmatches 838; Indels 964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50176; ARM REPEAT; 2.
2417 AA; 261282 MW; 08327727C475F254 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.1%; Score 1765; DB 5; 25.3%; Pred. No. 5.3e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AE003767; AAF56820.1; --
FlyBase; FBG00105589; Apc.
GO; 0008013; F:beta-catenin binding; IDA.
InterPro; IPR008938; ARM.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo.
SMART; SM00185; ARM; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                    VKD-----2258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2564 WRRIGSSSSILSASSESSEKAKSEDEKHVNSISGIKQSKENQVSAK--GIWRKIKENEFS 2621
                                      1898 İKPPSLMDELLDSMISVDSIQSEVADGEQDCSMATTISVSNYETAACDDQTMTVLQSCFD 1957
                                                                                                                                      2321
                                                                                                                                                                                                                       2078 AMMQOFTFITDINIGHSQETCESTDHPEDAGESPECDQNSETESCDGQEPDHLPPPPSIV 2137
                                                                                                                                                                                                                                                                                                                                             -----SNNAAPSKKKTLSPTIAKRSLVPGGSGVRLPAKKKPTPPPBPAPARLERQGTF 2230
                                                                                                                                                                                                                                                                                                                                                                                                                                    2504 WRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVST 2563
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                                                                                                   EDEDATMNDYSSAESTPKHGSTPSPNRRSLTPKDKRRLTKDRFKTYTIATSCEMBAPEAN 2017
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                                                                                                                                                     -------ISPPNKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2398 SKGLNOMNNGNGANKKVELSRMSSTKS----SGSESDRSERPV-----LVRQSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PINS---TSQTVSSGATNGAESKTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endoptera, Diptera; Brachycera; Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                  2138 DLRISVVKPTTLEPATAVKLVRGRKKPAYVSPYSMQSQRN------
                 MKQP-----LOANMPSISRGRIMIHIPGVRNSSSSTSPVSKKGPPL-
                                                                                                                                  QTSQI-----GGSSKAPSRSGSRDSTPSRPAQQPLSRPI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                          -----KTPASKSPSEGQTATTSPRGAKPSVKSEL-
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SEQUENCE FROM N.A.
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APC OR CG1451.
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	1685	EKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAEC
	1728	SLSSSQPIAINAATSASSLNSAMTVRKSQQQESYSSVDSSDSNDNQSKSLFELCILKGMY 1417
	76	<
	1802	ERVFSDNKDSK-KONLKONSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSR 1858 
	1859	NDSLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQPI 1918 
	1919	DAIATVTDTVRSPAAPNQGNGNASQNGLET-ATGSKDLPDRGAATDEKLQNFAIEN 1958
	1959	TPVCFSHNSSLSSLSDIDQENN 1980               : :           :
	1981	NKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSTDSEDD 2037
	2038	LLQECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRFDSEHGLS 2093
	2094	PDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKS 2140
	2141	GI-SLGSPFHLTPDQEEKFFTSNKGPRILKPGEKSTLETKKIESESKGIKGCKKVYKS 2197
	2198 1885	LITGKVRSNSEISGGMKQPLQANMPSISRGRTMHIPGVRNSSSSTSBVSKKGPP 2252
	2253	L
*	2283	SPVARQTSQI 2321
	2322	DODDICE STRAMMOPFITTDINIGHSORTCESTDHPEDAGESFECDONSETESC 2123
	2334	NGPRISSPSTKSSG   NGPRISSPSTKSSG 
	2383	GLSKNASSIPRSESASKGLNOMMNGNGANKKVELSRMSSTKSSGSESDRSERPV- 2436
	2437	LVRQSTFIXEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQTPVLSPSL 2488 

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QY 2489 PDMSLSTHSSVQAGGWRRLPPNLSPTIEYNDGRPAKHDIARSHSESPSRLPINRSGTWK 2548	PRESULT 10  QUENG  COURNEL  OUTD (SUENG  OINAY-2000 (TEXMELTE1. 13, Created)  DT 01-NAY-2000 (TEXMELTE1. 13, Last sequence update)  DT 01-NAY-2000 (TEXMELTE1. 13, Last sequence update)  DT 01-NAY-2000 (TEXMELTE1. 13, Last annotation update)  DT 01-NAY-2000 (TEXMELTE1. 13, Last annotation update)  DT 01-NAY-2000 (TEXMELTE1. 13, Last annotation update)  DT 01-NAY-2000 (TEXMELTE1. 13, Last annotation update)  DN 01-NAY-2000 (TEXMELTE1. 13, Last annotation update)  NE APCZ protein (Fragment).  SUMMARIA (TEXMELTE1. 13, Last annotation update)  NOT 1 (TEXMELTE1. 13, Last annotation update)  NOT 1 (TEXMELTE1. 13, Last annotation (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation) (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotation);  NOT 1 (TEXMELTE1. 13, Last annotatio	Query Match         11.7%; Score 1705; DB 4; Length 1685;           Best Local Similarity 28.5%; Pred. No. 2.9e-75;         Matches 641; Conservative 263; Mismatches 664; Indels 682; Gaps 86;           Qy         654 OILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNARDEALWDWGAVSMLKNLHS 713           Db         1 QVLRDHNCLQTLLQHLKSHSLTIVSNACGTLWNLSARSARDGELMDGAVGNLRNLLHS 713           Cy         714 KHXMIAMGARAALKKY-DANIMSPGSSLPSLHYRKQKALEAELDARLHLAVHS 60           Cy         714 KHXMIAMGSAAALRULAHRPAKK-DANIMSPGSSLPSLHYRKQRALEAELDARLHAAD 120           Cy         773 FDNIDNLSPKASHRSKQRHKQSLYGDYVFDTNRHDDRSDNFNTG	

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992	SKFCSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNSGRQSPSQNBRWAR	1051
325	LPPLASTREDP	339
1052	PKHIIEDEIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQQECVSPYRSRGANGSE	1111348
1112	TNRVGSNHGINQNVSQSLCQEDDYEDDKPTNYSERYSEBEQHEBEERPTNYSIKYNEEKR	1171
1172 383	HVDQPIDYSLKYATDIPSSOKQSFSFSKSSSGQSSKTEHMSSSSENTSTPSSNAKRQNQL 	1231
1232	HPSSAQSRSGQPQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSAEDEIGCNG	1291 468
1292	TTQEADSANTLQIAEIKEKIGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSS GGDLDDSDSSLEGLEEAGFSEAELDSTWRAPGATSLPVAIPAPRRNRGRGLG	1344 520
1345	ESARHKAVEFSSGAKSPSKSGAQTPKSPPEHYVOETPLMFSRCTSVSSLDSFESRSIASS	1404 561
1405	VQSEPCSGMVSGIISPSDLPDSPQTMPPSRSKTPPPPPQTAQTKREVPKNKAPTAEK :	1462 614
1463	RESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSSLSALSLDEPFIQKD	1519 673
1520	VELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSEKDLLDDSDDDJEILEECI	1579 729
1580	ISAMPTKSSRKAKKPAQTASKLPPPVARKPSQLPVYKLLPSQNRLQPQKHVSFTPGDDMP:	1639
1640	RVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQSGEFEKRDTIPTEGRSTDE	1699 817
1700	AQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSA 	1759 833
1760	PNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLNAERVFSDNKD :::	1810 862
1811	SKKQNLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRNDSLSSLDFDDD	1870 896
1871	DVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQPINRGQPKPILQKO	1930
1931	STEPQSSKDIPDRGAATDEKLQ-NFAIENTPVCFSHNSSLSSLSDIDQENNNKENEPIKE	1989 973

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EAERSSOSRHDAASHEAGRQHEGHGVAESNTAASSSGQ 276
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31.4%; Pred. No. 6.1e-54;
[ve 8; Mismatches 14;
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Matches 254; Conservative
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01-NOV-1999 (TrEMBLrel. 12,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                   EEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMK 2214
                                                                                                                                                                                                                1123 ABGEMGSARRP-----BKRCAASVKTSGSPRSPAGPEK-------PRGT 1159
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   TEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPK 2049
                 1066 VEWRAIQEGANSIVTWLAQAAAA---TREASSESDSILSFVSGLSVGSTLQPPKHRKGRQ
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                                                                                                                        2009 FDWKAIQEGANSIVSSIHQAAAAACLSRQASSDSDSILSLKSGISLGS----PFHLTPDQ
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI TaxID=10090,
                                                             1050 KKKP-SRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRP---DSEHG-
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01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
Adenomatosis polyposis coli.
Mus musculus (Mouse).
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RESULT 11

OCCEPTED

PEQUENCE FROM N.A.

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C STRAIN=CSTSH460; TISSUB=Cerebellum;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA The FANTOM Consortium,

RA The RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of FT "Analysis of the mouse transcriptome based on functional annotation of RT 60,770 full-length cDNas.";

RL Nature 420:563-573(2002).

RL Nature 420:563-573(2002).

RE MBL; AKO82724; BAC38587.1; --
REDIBL; AKO82724; BAC38587.1; --
REQUENCE 324 AA; 36909 MW; D74E29ECD952DICC CRC64;

REQUENCE 324 AA; 36909 MW; ARECOUNTE 1252; DB 11; Length 324; STRAIN=Berkeley;

X MEDLINE=20196006; PubMed=10731132;

Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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A challey B., Delcher A., Deng Z., Mays A.D., S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Fleischmann W.,
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Botts C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
A dlodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., 2; ASSGQIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR 120 118 180 RIFVNGSRESTGYLEELEKERSLILADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL 178 240 9 9 1 MAAASYDQLLKQVBALKMBNSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDETM - TSGQIDLLERLKEFNID-SNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR QTDMTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT 1 MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM 121 RGFVNGSRESTGYLEELEKERSLILLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilae; Drosophila.

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A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., A Kimmel B.E., Kodirac C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Lid J. Liang Y., Lin X., A Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., A McKulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., She B.C., Stden-Kiamos T., Simpson M., Skupski M.P., Smith T., RA Shier B.C., Stden-Kiamos T., Simpson M., Skupski M.P., Smith T., Syier B., Tector C., Turner R., Wenter E., Wang X., Smith T., Shier S., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., A Zheng X.H., Zhong F.W., Zhou K., Zhu S., Zhao Q., Zheng L., Ra Zheng X.H., Zhong F.W., Zhou K., Zhu S., Zhu X., Smith H.O., Ra Zheng X.H., Myers E.W., Rubin G.M., Venter J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Yu X., Bienz M.; "A new Drosophila APC homolog concentrated in apical adhesion zones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.4%; Score 1222.5; DB 5; Length 1067; 26.3%; Pred. No. 8.6e-52; ive 178; Mismatches 379; Indels 647;
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SWART; SM00185; ARW; 6.
PROSITE; PS50176; ARM REPEAT; 1.
SEQUENCE 1067 AA; 116702 MW;
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InterPro; IPR008938; ARM.
InterPro; IPR000225; Armadillo.
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Curr. Biol. 9:105-108(1999).

EMBL; AE003746, ARE56249.1; --

EMBL; AF113913; AAD40227.1; --

EMBL; AF01430; AAD20985.2; --
                                                                                                                                                                                                                                                                                                                                                                 Science 287:2185-2195(2000).
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Nat. Cell Biol. 0:0-0(1999).
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SEQUENCE FROM N.A.
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bb 925 RIPPKEDSLSSLSMDSDDDCNLLSCAIAAGSCRPOPSGA 964	1787 TRVRKNADSKONLNAERVFSDNKDSKKQNLKONSKDFNDKLFNNEDRVRG	Qy 1847 TPIEGTPYCESRNDSLSSLDFDDDDVDLSREKAELRKAKENKESEA 1892 	Qy 1893 -KVTSHTELTSNQ 1904		RESULT 13 Q961B0 PRELIMINARY; PRT; 1067 AA. ID Q961B0 PRELIMINARY; PRT; 1067 AA.	0961B0; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence		OS Drosophila melanogaster (Fruit fly). OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		[1] SEQUENCE FROM N.A.	STRAIN=Berkeley; Stapleton M., Brokstein P., Hong L.		RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. DR EMBL; AY051719; AAK93143.1; DR Flybase; FBgn0026598; Apc2.		SMART PROSIT SEQUE	Query Match 8.4%; Score 1221.5; DB 5; Length 1067; Best Local Similarity 26.3%; Pred. No. 9.7e-52; Marches 429; Conservative 178; Mismatches 379; Indels 647; Gaps 50;	329 DMSRTLLAMSSSQDSCISMRQSGCLPLLIQLHGNDKDSVLLGNSRGSKEARARA :::	SAHEP-GMDQDKNPMPAPVEHQI	Db 63 NIVHNNPEEKERQREVKMLRLLDQILDYCNFLHTQLQSGGBAIADDEDRHPL 114	OY 447 CPAVCVIMKLSFDEEHRHAMNELGGLQAIAELLQVDCEMYG-LTNDHYSITLRRYAGMAL 505    :	TNLTFGDVANKATLCSMKGCMRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTL	174	OY REVISIONAL MECHANISM OF THE NATIONAL STATES AND AN AN AN AN AN AN AN AN AN AN AN AN AN	Qy 624 SQTNTLAIIESGGGILRNVSSLIATNEDHRQILRENNCLQTLLQHLKSHSLTIVSNACGT 683

LDDNK-AEEGDILAECINS 1730 SERYSEREQHEEEERPTNYS 1163 LPDSPGQTMP--PSRSKTP 1439 VLPDADTLLHFATESTPDG 1499 FSKSSSGQSSKTEHMSSSS 1215 ATCKVSSINGETIQTYCVE 1265 IKEKIGTRSAEDPVSEVPA 1325 OTPKSPPEHYVOETPLMFS 1385 QPKESNENQE-KEAEKŢID 1558 KLPPPVA-----RKPSQ 1611 TATSLSDLTIESPPNELAA 1671 INYSLKYSDEQLNSGROSP 1043 KHLKFQPHFGQQECVSPYR 1103 |||||| |:|| LPDSPTQSMPQSPRRDR-- 716 :| | | : PVPAPRADVTGMDTRMPAE 841 :| | ------TEKPE 623 NTPQNIDS--ALETPLMFS 660 ----DKLNRFHVEHTPAA 750 RGNDINGNGDAPRSYCTED 793 : || ||: VISGLSHLTV----- 887 : | | ::: | :: --KERRSAQTAQPELKSETN 551 || : : | | | | | AT-ETETAERPINYCEE 603 ---STKYST---- 482 -----K 483 ALRULMANRPAKYKDANIM 743 ||:||: | : | ALKNLVNFRATQELMPN-- 411 HRSKQRHKQSLYGDYVFDT 803 RSEKDRSLERERGIGLGNY 863 SSGSTTELHCVTDERNALR 923 NSVSSSDGYGKRGOMKPSI 983 :||:: :: || -TVSTTGFLNRKCESRESI 470 -----LDKBAGHG---- 426 432

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completed: August 25, 2004, 17:23:07
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----GSAKAGPVLK---LPM--RTAEEAQA------PKLPPRRSAVQGD----AEP 924
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                                                                                                                                                                    965 ----STSSSLANASTSTLCRENGQSKKQ-----VEHGDK-PN-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Adenomatosis polyposis coli tumor suppressor (Fragment).
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208 AA; 22726 MW; 51076F257B61C528 CRC64;
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Hum. Genet. 106:101-107(2000).

EMBL; AF127506; AAF34355.1; -.

EMBL; AF127034; AAF34355.1; JOINED.
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InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 2.
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159 AA

PRT;

PRELIMINARY;

Q7Z2Q8 Q7Z2Q8;

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MEDLINE=22388257 PubMed=12477932;

MEDLINE=22388257 PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Riabserg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McKwan P.J., McKerran K.J., Mallek J.A., Gunzarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Radinges S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevolcheko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

H. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ASSGQIDLLERLKELNLDSSNFPGVKLRSKWSLRSYGSREGSVSSRSGECSPVPMGSFPR 120
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Eukaryota; Metazona; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC056268; AAH56268.1; -
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NON TER 159 159
SEQUENCE 159 AA; 17843 MW; E0COCCO55A22C91B CRC64;
                                                 Last sequence update)
Last annotation update)
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        Created)
01-OCT-2003 (TrEMBLrel. 25, Creat O1-OCT-2003 (TrEMBLrel. 25, Last O1-OCT-2003 (TrEMBLrel. 25, Last Hypothetical protein (Fragment). Homo sapiens (Human).
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Best Local Similarity 98.7
Matches 153, Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 25, 2004, 16:58:01; Search time 180.5 Seconds (without alignments) 4450.319 Million cell updates/sec Run on:

US-09-442-489F-7 14566 1 MAAASYDQLLKQVEALKMEN.......ESSGTQSPKRHSGSYLVTSV 2843 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqp2000s:\* geneseqp2001s:\* geneseqp2001s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* A\_Geneseq\_29Jan04:\* 1: geneseqp1980s:\* 2: geneseqp1990s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ΙD	AAW76140	AAW76144	AAB23011	ABG71105	AAW76821	AAY72782	AAY70304	AAR63508	ABG90968	AAW11922	ADE65846	AAR26052	AAW35392	AAW38370	ABG90964	AAR63507	AAR58634	AAB23012	ADE56175	ABG71106	ABG71107	AAB50674	ABG09335	ABR58648	AAY92061
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## ALIGNMENTS

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Familial adenomatous polyposis coli, APC; tumour suppressor; therapy; chromosome 5q21; tumourigenesis; retinoblastoma; colorectal tumour; FAP; Gardner's Syndrome; GS; predisposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Adenomatous polyposis coli protein - useful in the treatment of cancers associated with mutation(s) on human chromosome 5q21.
                                                                                                                                                                                                                                                                                                                                                               White RL;
Albertsen H;
                                                                                                                                                                                                                                                                                                                                                               , Carlson M,
Nakamura Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Col 41-54; 102pp; English.
                   AAW76140 standard; protein; 2843 AA
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Thliveris A, Groden J, Anand R,
Vogelstein B, Hedge PJ;
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91GB-0000963.
91GB-0000974.
91GB-0000975.
91US-00741940.
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                                                                                                                                                                                                                                                                                                          (CANC-) CANCER INST.
(UYJO ) UNIV JOHNS HOPKINS.
(UTAH ) UNIV UTAH.
(ZENE ) ZENECA PHARM.
                                                            (revised)
(first entry)
                                                                                          Human APC protein #1.
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N-PSDB; AAV56447.
                                                                                                                                                                                                                                    16-JAN-1991;
16-JAN-1991;
16-JAN-1991;
16-JAN-1991;
08-AUG-1991;
12-AUG-1994;
                                                            25-MAR-2003
23-NOV-1998
                                                                                                                                                        Homo sapiens
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                                                                                                                                                                          US5783666-A.
                                                                                                                                                                                              21-JUL-1998
                                        AAW76140;
RESULT 1
AAW76140
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This sequence represents a human familial adenomatous polyposis coli

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human chromosome 5q1 and is also referred to as adenomatous polyposis coli gene. It is a tumour suppressor gene, and mutations in this gene have been associated with tumourigenesis in retinoblastoma and colorecta tumours, and especially familial adenomatous polyposis (FAP) and Gardner's Syndrome (GS). The protein can be used in therapy to replace lack of native functional protein and the nucleic acids can be used for gene therapy. The nucleic acids that encode them can also be used for probes and primers in detection of the cancers and predisposition to it. (Updated on 25-MAR-2003 to correct PR field.)  Sequence 2843 AA;  Duery Match  100.0%; Score 14566; DB 2; Length 2843;  Best Local Similarity 100.0%; Pred. No. 0;	Matches 2843; Conservation () Hismatches 2843; Conservation () Mismatche 1 Mahasydollkovealkmensulroelednsn	121 RGFVNGSRESTGYLEELEXERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL 180  121 RGFVNGSRESTGYLEELEXERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL 180  121 RGFVNGSRESTGYLEELEXERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL 180  181 QTDMTRRQLEYEARQIRVAWEEQLGTCODWEKRAQRRIARIQQIEKDILRIRQLLQSQAT 240  181 QTDMTRRQLEYEARQIRVAWEEQLGTCODWEKRAQRRIARIQQIEKDILRIRQLLQSQAT 240  241 EAERSSQNKHFTGSHDAERQNEGGGVGEINMATSGNGGSTTRWDHETASVLSSSSTHSA 300  241 EAERSSQNKHFTGSHDAERQNEGGGVGEINMATSGNGGSTTRWDHETASVLSSSSTHSA 300	301 PRRITSHIGTKVEMYYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLIQLL 360 301 PRRLTSHLGTKVEMYYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLILIQLL 360 361 HGNDKDSVLLGNSRGSKEARARASAALHNIHSQPDDKRGRREIRVLHLLEQIRAYCETC 420 361 HGNDKDSVLLGNSRGSKEARARASAALHNIHSQPDDKRGRREIRVLHLLEQIRAYCETC 420 421 WEWQEAHEPGMDQDXDPMPAPVEHQICPAVCVLMKLSFDEEHRHANNELGGLQAIAELLQ 480 421 WEWQEAHEPGMDQDXNPMPAPVEHQICPAVCVLMKLSFDEEHRHANNELGGLQAIAELLQ 480		661 CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDWGAVSMLKNLHSKHKMIAM 720 [1
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දු පු	841	LDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVWEEVSAIHTS 900 
දු පු	901	QEDRSGGSTTELHCVTDERNALRRSSAAHTHSNITNFTKSENSNRICSMPYAKLEYKRSS 960 
ර සි	961	SLNSVSSSDGYGKRGOMKPSIESYSEDDESKFCSYGOYPADLAHKIHS 
જે વૃ	1021	SPSQNERWARPKHIIEDEIKQSEQRQSRNQSTTYPVYTE 108
è a	1081	SIDDKHLKROPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKP 1140 
è a	1141	EQHEBEERPTNYSIKYNESKRHVDQPIDYS 
S d	1201	SNTSTPSS          SNTSTPSS
Š S	1261	TYCVEDTPICFSRCSSLSSLSSAEDEIGCNQTTQEADSANTLQIAEIKEKIGTRSAEDPV 1320 
දු දු	1321	RHKAVE        RHKAVE
දු දු	1381	PLMFSRCTSVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPP 1440 
\ <del>Q</del>	1441	KREVPKNKAPTAEKRES
δγ Op	1501	SLSALSLDEPFIQKOVELRIMPPVQENDNGNE 
\$ &	1561	DDIEILEECTISAMPTKSSRKAKKPAQTASKLPPVV 
S S	1621	RLOPOKHVSFTPGDDMPRVYCVBGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 168 
çy O	1681	SKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKP 174
පු දු	1741	VKKIMDQVQQASASSSAPNKNQLDGKKKKPTSPVKFIPQNTEYRTKVRKNADSKANLN 1 
දු දු	1801	CKQNLKNNSKDFNDKLPNNEDRVRGSFAF                   CKQNLKNNSKDFNDKLPNNEDRVRGSFAF
δλ	86	SLDFDDDVDLSREKAELRKAKENKESBAKVTSHTELTSNQSANKTO
a &	1861	SSLDFDDDDVDLSKEKAELKARANENKESEAKVISHIEDISNQQSANALQALANALFINA 1918 FKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSDIDQENN 198

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This sequence represents a human familial adenomatous polyposis coli (APC) protein isolated from 87 cDNA clones. The gene for the protein is present on human chromosome 5q21 and is also referred to as adenomatous polyposis coli gene. It is a tumour suppressor gene, and mutations in this gene have been associated with tumourigenesis in retinoblastoma and colorectal tumours, and especially familial adenomatous polyposis (PAP) and Gardner's Syndrome (GS). The protein can be used in therapy to replace lack of native functional protein and the nucleic acids can be used for gene therapy. The nucleic acids that encode them can also be used as probes and primers in detection of the cancers and predisposition to it. (Updated on 25-MAR-2003 to correct PR field.)
                             Familial adenomatous polyposis coli, APC, tumour suppressor; therapy, chromosome 5q21; tumourigenesis, retinoblastoma, colorectal tumour; FAP; Gardner's Syndrome; GS; predisposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2843;
                                                                                                                                                                                                                                                                                                                                                                                                            Adenomatous polyposis coli protein - useful in the treatment associated with mutation(s) on human chromosome 5q21.
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Albertsen 1
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R, Nakamura Y,
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100.0%; Score 14566;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2843; Conservative 0; Mismatches
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Thliveris A, Groden J, Anand
Vogelstein B, Hedge PJ;
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16-JAN-1991;
16-JAN-1991;
08-AUG-1991;
12-AUG-1994;
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                                                                                                      ECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD
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LPHKNOLDGKKKKPTSPVKPIPQNTZYTRVRKNADSKONLN |||||||||||||||||||||| \text{Approcedents of the point synth vrknadskonln} NNEKHSPRNMGGILGEDLTLDLKDIORPDSEHGLSPDSENFD RVYCVBGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAO KKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQPLQAN SSSSTSPVSKKGPPLKTPASKSPSEGQTATTSPRGAKPSVKS SGSGKMSYTSPGROMSQQNLTKQTGLSKNASSIPRSESASKG VVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSE SKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRND 48KDFNDKLPNNEDRVRGSFAFDSPHHYTF1EGTPYCFSRND AAACLSRQASSDSDS1LSLKSGISLGSPFHLTPDQEEKPFT CKIESESKGIKGGKKVYKSLITGKVRSNSEISGOMKQPLQAN SSSTSPVSKKGPPLKTPASKSPSEGQTATTSPRGAKPSVKS SERSGSRDSTPSRPAQOPLSRPIQSPGRNSISPGRNGISPPN SIASSVQSEPCSGWVSGIISPSDLPDSPGQTMPPSRSKTPP AQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKP AAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPFT A SEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGF 

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                          SFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEVNDG
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A, Nakamura Y, Vogelstein B;
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The invention relates to a novel method for detecting Adenomatous

C Polyposis Coli (APC) protein in a sample. The method involves contacting

C the sample with antibodies which specifically binds to the 2843 amino

acid form of the human APC protein, or to a mutant APC protein, and

detecting an APC-antibody complex. Mutations in the APC gene play a role

CC in tumorigenesis, indicating that it is a tumour suppressor gene. It is

CC located on chromosome 5q21, which corresponds to the PAP (familial)

adenomatous polyposis) locus. FAP is an autosomal dominant inherited

disease in which affected individuals develop hundreds to thousands of

adenomatous polyps in the colon and rectum, some of which progress to

calenomatous polyps in the colon and rectum, some of which progress to

calenomatous polyps in the colon and rectum, some of which progress to

complement and the FAP locus is often found to be deleted in sporadic (i.e.,

complemental rissue, stomach, and prostate, and in leukaemias and

complemental rissue, and MCC, it is thought that mutations in the APC gene play

can key role in the development of FAP and sporadic tumours. The method is

cuseful for detecting APC protein and its mutant forms in foetal tissue,

constitute alteration of wild-type APC genes, and for testing therapeutic

condition alteration of wild-type APC genes, and for testing therapeutic

condition alteration of wild-type APC genes, and for testing therapeutic

condition alteration of wild-type APC genes, and for testing therapeutic

condition alteration of wild-type APC genes, and for testing therapeutic

capants for the ability to suppress tumours. The present sequence

crepresents a 2843 amino acid splice variant of the human APC protein.

This variant is more abundant than the 2742 amino acid variant (AAB23012)
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Detecting Adenomatous Polypopsis Coli (APC) protein in a sample for diagnosing cancers, involves contacting the sample with antibodies that specifically bind to APC protein and detecting the complex formed.
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100.0%; Score 14566;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2843; Conservative 0; Mismatches
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                                                                                                         QTDMTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRIARIQQIEKDILRIRQLLQSQAT
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                                                  RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL
                                                                                     QTDMTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT
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                       RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL
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1201 SSGQSSKTEHMSSSENTSTPSSNAKRONOLHPSSAGGREGOPGKAATCKVSSINGETTQ 1260	1801 AERVFSDNKDSKKORLKNNSKDFNDKLPNNBDRVRGSFAFDSPHHYTPIEGTPYCFSRND 1860 1801 AERVFSDNKDSKKORLKNNSKDFNDLLPNNBDRVRGSFAFDSPHHYTPIEGTPYCFSRND 1860 1801 AERVFSDNKDSKKORLKNNSKDFNDLLPNNBDRVRGSFAFDSPHHYTPIEGTPYCFSRND 1860 1801 SLSSLDFDDDDVDLSREKAELRKAKENKESBAKVTSHTELTSNOQSANKTQAIAKQPINR 1920 1921 GQPKPILOKOSTFPOSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSDIDGENN 1980 1921 GQPKPILOKOSTFPOSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSDIDGENN 1980 1981 NKENEPIKETFPPDSQGFPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSBDDLLQ 2040 1981 NKENEPIKETFPPDSQGFPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSBDDLLQ 2040 1981 NKENEPIKETFPPDSQGFPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSBDDLLQ 2040 2041 ECISSAMPKKKRSRLKGDNEKHSPRNMCGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKRSRLKGDNEKHSPRNMCGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKRSRLKGDNEKHSPRNMCGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKRSRLKGDNEKHSPRNMCGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKRSRLKGDNEKHSPRNMCGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKRSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKRSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKRSTLKRDEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKRSTLKRDEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKRSTLKRDEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKRSTLIKPTRABARAGSSDSSILSKKSGISGSFHILTPDQEEKFFT 2160 2101 WKALQEGANSTUSFKRGPRNMGGILGEDLTLDLKFYRSNSEISGQWKQPLQAN 2220 211 MFALGERNSTLIFFREESEKGIRGGKKVYKSLLITGKVRSNSEISGQWKQPLQAN 2220 212 MPSISRGRTMIHIPGVRNSSSTSPVSKKGPPLKTPASKSPSEGGTATTSPRGAKPSVKS 2280 2221 MPSISRGRTMIHIPGVRNSSSTSPVSKKGPPLKTPASKSPSEGGTATTSPRGAKPSVKS 2280 2221 MPSISRGRTMIHIPGVRNSSSTSPVSKKGPPLKTPASKSPSEGGTATTSPRGAKPSVKS 2280 2221 MPSISRGRTMIHIPGVRNSSSTSPVSKKGPPLKTPASKSPSEGGTATTSPRGAKPSVKS 2280 2221 MPSISRGRTMIHIPGVRNSSSTSPVSKKGPPLKTPASKSPSEGGTATTSPRGAKPSVKS 2280 2221 MPSISRGRTMIHIPGVRNSSSTSPVSKKGPPLKTPASKSPSEGGTATTSPRGAKPSVKS 2280 2221 MPSISRGRTMHIRPGVRNSSSTSPVSKKGPPLKTPASKSPSEGGTATTSPRGAKPSVKS 2280 2221 MSISRGRTMHIRPGVRNSSS

cancer developing Disclosure, Page 32-37; 58pp; English.

This sequence represents a human APC protein which is used in a method of identifying candidate drugs for use in familial adenomatous polyposis (FAP) patients, or patients with increased risk of developing cancer. The protein can also be used to determine the presence or absence in a cell of wild type adenomatous polyposis coli (APC) gene or a downstream introducing a Tcf-responsive reporter gene into the cell, and measuring introducing a Tcf-responsive reporter gene into the cell, and measuring transcription of the reporter gene does not have wild type APC or a downstream protein of the PAPC transcription regulatory pathway. The construction of the APC transcription regulatory pathway. The construction of the APC transcription regulatory pathway. The construction of the APC transcription regulatory pathway. The construction of the APC transcription regulatory pathway. The conspected of being neoplastic and for treating a patient with colorectal cancer or other cancer associated with FAP, comprising administering to the patient a polypeptide comprising a portion of the APC sequence, comprising the beta-catenin binding site 

Sequence 2973 AA;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2843; Conservative 0; Mismatches 61 61 121 121 181 301 181 241 241 301 361 361 421 481 481 541 541 601 601 661

1560 1560 960 GSAAALRNLWANRPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLS PKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSRGS LDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHIIEDBIKQSEQRQSRNQSTTYPVYTE LDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTS LOSSESESEKDESLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTS TNYSERYSEEEQHEEEERPTNYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSKS PKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSRGS QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS LDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHIIEDEIKQSEQRQSRNQSTTYPVYTE STDDKHLKFQPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKP STDDKHLKFQPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKP NDSLNSVSSSDGYGKRGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGE TNYSERYSEBEQHEBEERPTNYSIKYNBEKRHVDQPIDYSLKYATDIPSSQKQSFSFSKS SSGQSSKTEHMSSSSENTSTPSSNAKRONOLHPSSAQSRSGOPOKAATCKVSSINQETIQ SEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFSSGAKSPSKSGAQTPKSPPEHYVQET TYCVEDTPICFSRCSSLSSAEDEIGCNOTTOBADSANTLOIAEIKEKIGTRSAEDPV TYCVEDTPICFSRCSSLSSLSSAEDEIGCNQTTQEADSANTLQIAEIKEKIGTRSAEDEPV SEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFSSGAKSPSKSGAQTPKSPPEHYVQET PLMFSRCTSVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPP PPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGF SCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSE QNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAO SGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKP PPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGF SCSSSLSALSLDEPFIQXDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSE KDLLDDSDDDDIBILBECIISAMPTKSSRKAKKPAQTASKLPPPVARKPSQLPVYKLLPS KDLLDDSDDDDIBILEECIISAMPTKSSRKAKKPAQTASKLPPPVARKPSQLPVYKLLPS **ONRLOPOXHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ** SGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKP FRVKKIMDQVQQASASSSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLN FRVKKIMDQVQQASASSSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKANLN 721 1501 1021 1081 1141 1261 1441 721 781 781 841 901 196 961 1021 1081 1141 1201 1201 1261 1321 1321 1381 1381 1441 901 1501 1561 1561 1621 1621 1681 1681 1741 1741 ð : 음 g & õ qq 8 d ò 음 상 음 \$ 8 \$ 성 유 셤 8 & 8 & 8 8 8 g ò g 셤 ò 8 셤 ð

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The present sequence is a transcriptional activation protein related to the invention. The invention relates to human Tcf-4 proteins and their corresponding CDNA molecules which encodes transcriptional activation factorized to the content and activation in Colorecal epithelial cells. Moreover it has cativates transcription in Colorecal epithelial cells. Moreover it has been found that adenomatous polyposis coli (APC) regulates this content also provides a recombinant adenovirus, Ad-Mini-Me ie., APC Minus its also provides a recombinant adenovirus, Ad-Mini-Me ie., APC Minus its camino- and carboxyl -terminal Ends which expresses a fusion protein, cy green fluorescent protein (EPP)/CAPC containing GFP fused to the central caper fluorescent protein (EPP)/CAPC containing GFP fused to the central condition apoptosis or treating colorectal cancer. These fusion proteins care useful for treating cancer, e.g. colorectal cancer, and other cancers associated with Familial Adenomatous Polyposis (FAP) or patients with increased risk of developing cancer. Human Tcf-4 CDNA provides an excellent system for screening agents for their ability to promote callivery, integration, hybridization, expression, replication or integration in cells or in a nample suspected of being neoplastic
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                                                                                                                                              Human, Tcf-4 protein; transcriptional activation factor; beta-catenin; apoptosis; colorectal cancer; Familial Adenomatous Polyposis; FAP; APC; adenomatous polyposis coli; recombinant adenovirus; Ad-Min1-Me; therapy; GFP; green fluorescent protein; GFP/cAPC fusion protein; cytostatic.
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                                                                                                         Transcriptional activation protein #1 related to the invention.
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Adenomatous polyposis coli; APC; transcriptional activation;
For responsive reporter gene, APC transcription regulatory pathway;
familial adenomatous polyposis; FAP; cancer; colorectal; thyroid; brain;
medulloblastoma; breast; head; neck; desmoid tumour; osteoma; cytostatic.
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                     KLSQLPRISSPSTASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKNASSIPRSESASKG
                                                                               SFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDG
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100.0%; Score 14559;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2842; Conservative 0; Mismatches
Disclosure; Page 58-65; 70pp; English.
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